



SEQUENCE LISTING

<110> Kato, Seishi et al.

<120> HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND DNAs
ENCODING THESE PROTEINS

<130> GIN-6705CPUS

<140> 09/284,320

<141> 1999-04-28

<150> JP 8-301429

<151> 1996-11-13

<150> PCT/JP97/04056

<151> 1997-11-07

<160> 90

<170> PatentIn Ver. 2.0

<210> 1

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<213> Homo sapiens

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35 40 45
Trp Ser Asn Leu Gly Ile Gly Leu Ala Ile Ser Leu Ser Val Val Gly
50 55 60
Ala Ala Trp Gly Ile Tyr Ile Thr Gly Ser Ser Ile Ile Gly Gly Gly
65 70 75 80
Val Lys Ala Pro Arg Ile Lys Thr Lys Asn Leu Val Ser Ile Ile Phe
85 90 95
Cys Glu Ala Val Ala Ile Tyr Gly Ile Ile Met Ala Ile Val Ile Ser
100 105 110
Asn Met Ala Glu Pro Phe Ser Ala Thr Asp Pro Lys Ala Ile Gly His
115 120 125
Arg Asn Tyr His Ala Gly Tyr Ser Met Phe Gly Ala Gly Leu Thr Val
130 135 140
Gly Leu Ser Asn Leu Phe Cys Gly Val Cys Val Gly Ile Val Gly Ser
145 150 155 160

Gly Ala Ala Leu Ala Asp Ala Gln Asn Pro Ser Leu Phe Val Lys Ile
165 170 175

Leu Ile Val Glu Ile Phe Gly Ser Ala Ile Gly Leu Phe Gly Val Ile
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Val Ala Ile Leu Gln Thr Ser Arg Val Lys Met Gly Asp
195 200 205

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Ala Gln Pro Pro Tyr Pro Gly Ala Pro Tyr Pro Gln Pro Pro Phe Gln
35 40 45

Pro Ser Pro Tyr Gly Gln Pro Gly Tyr Pro His Gly Pro Ser Pro Tyr
50 55 60

Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro
65 70 75 80

Gln Gly Pro Tyr Pro Gln Glu Gly Tyr Pro Gln Gly Pro Tyr Pro Gln
85 90 95

Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Ser Pro Phe Pro Pro Asn
100 105 110

Pro Tyr Gly Gln Pro Gln Val Phe Pro Gly Gln Asp Pro Asp Ser Pro
115 120 125

Gln His Gly Asn Tyr Gln Glu Glu Gly Pro Pro Ser Tyr Tyr Asp Asn
130 135 140

Gln Asp Phe Pro Ala Thr Asn Trp Asp Asp Lys Ser Ile Arg Gln Ala
145 150 155 160

Phe Ile Arg Lys Val Phe Leu Val Leu Thr Leu Gln Leu Ser Val Thr
165 170 175

Leu Ser Thr Val Ser Val Phe Thr Phe Val Ala Glu Val Lys Gly Phe
180 185 190

Val Arg Glu Asn Val Trp Thr Tyr Tyr Val Ser Tyr Ala Val Phe Phe
195 200 205

Ile Ser Leu Ile Val Leu Ser Cys Cys Gly Asp Phe Arg Arg Lys His

210 215 220
Pro Trp Asn Leu Val Ala Leu Ser Val Leu Thr Ala Ser Leu Ser Tyr
225 230 235 240
Met Val Gly Met Ile Ala Ser Phe Tyr Asn Thr Glu Ala Val Ile Met
245 250 255
Ala Val Gly Ile Thr Thr Ala Val Cys Phe Thr Val Val Ile Phe Ser
260 265 270
Met Gln Thr Arg Tyr Asp Phe Thr Ser Cys Met Gly Val Leu Leu Val
275 280 285
Ser Met Val Val Leu Phe Ile Phe Ala Ile Leu Cys Ile Phe Ile Arg
290 295 300
Asn Arg Ile Leu Glu Ile Val Tyr Ala Ser Leu Gly Ala Leu Leu Phe
305 310 315 320
Thr Cys Phe Leu Ala Val Asp Thr Gln Leu Leu Leu Gly Asn Lys Gln
325 330 335
Leu Ser Leu Ser Pro Glu Glu Tyr Val Phe Ala Ala Leu Asn Leu Tyr
340 345 350
Thr Asp Ile Ile Asn Ile Phe Leu Tyr Ile Leu Thr Ile Ile Gly Arg
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Ala Lys Glu
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35 40 45
Ile Val Val Val Leu Ser Gly Ser Met Glu Pro Ala Phe His Arg Gly
50 55 60
Asp Leu Leu Phe Leu Thr Asn Arg Val Glu Asp Pro Ile Arg Val Gly
65 70 75 80
Glu Ile Val Val Phe Arg Ile Glu Gly Arg Glu Ile Pro Ile Val His
85 90 95

Arg Val Leu Lys Ile His Glu Lys Gln Asn Gly His Ile Lys Phe Leu
100 105 110

Thr Lys Gly Asp Asn Asn Ala Val Asp Asp Arg Gly Leu Tyr Lys Gln
115 120 125

Gly Gln His Trp Leu Glu Lys Lys Asp Val Val Gly Arg Ala Arg Gly
130 135 140

Phe Val Pro Tyr Ile Gly Ile Val Thr Ile Leu Met Asn Asp Tyr Pro
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Lys Phe Lys Tyr Ala Val Leu Phe Leu Leu Gly Leu Phe Val Leu Val
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His Arg Glu

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35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu
50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu
65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys
85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr
100 105 110

Asp Cys Ser His Glu Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu
115 120 125

Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro
130 135 140

Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr
145 150 155 160

Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys
165 170 175

Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn
180 185 190

Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys
195 200 205

Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly
210 215 220

Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp
225 230 235 240

Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg
245 250 255

Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn
260 265 270

Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly
275 280 285

Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly
290 295 300

Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln
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325 330 335

His Gln Glu Asp Val Ala Val Ile Cys Ser Gly
340 345

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Ala Pro Ile Cys Val Gly Ile Val Phe Leu Gly Phe Thr Pro Asp His
35 40 45

His Cys Gln Ser Pro Gly Val Ala Glu Leu Ser Gln Arg Cys Gly Trp
50 55 60

Ser Pro Ala Glu Glu Leu Asn Tyr Thr Val Pro Gly Leu Gly Pro Ala
65 70 75 80

Gly Glu Ala Phe Leu Gly Gln Cys Arg Arg Tyr Glu Val Asp Trp Asn

85

90

95

Gln Ser Ala Leu Ser Cys Val Asp Pro Leu Ala Ser Leu Ala Thr Asn
100 105 110

Arg Ser His Leu Pro Leu Gly Pro Cys Gln Asp Gly Trp Val Tyr Asp
115 120 125

Thr Pro Gly Ser Ser Ile Val Thr Glu Phe Asn Leu Val Cys Ala Asp
130 135 140

Ser Trp Lys Leu Asp Leu Phe Gln Ser Cys Leu Asn Ala Gly Phe Phe
145 150 155 160

Phe Gly Ser Leu Gly Val Gly Tyr Phe Ala Asp Arg Phe Gly Arg Lys
165 170 175

Leu Cys Leu Leu Gly Thr Val Leu Val Asn Ala Val Ser Gly Val Leu
180 185 190

Met Ala Phe Ser Pro Asn Tyr Met Ser Met Leu Leu Phe Arg Leu Leu
195 200 205

Gln Gly Leu Val Ser Lys Gly Asn Trp Met Ala Gly Tyr Thr Leu Ile
210 215 220

Thr Glu Phe Val Gly Ser Gly Ser Arg Arg Thr Val Ala Ile Met Tyr
225 230 235 240

Gln Met Ala Phe Thr Val Gly Leu Val Ala Leu Thr Gly Leu Ala Tyr
245 250 255

Ala Leu Pro His Trp Arg Trp Leu Gln Leu Ala Val Ser Leu Pro Thr
260 265 270

Phe Leu Phe Leu Leu Tyr Tyr Trp Cys Val Pro Glu Ser Pro Arg Trp
275 280 285

Leu Leu Ser Gln Lys Arg Asn Thr Glu Ala Ile Lys Ile Met Asp His
290 295 300

Ile Ala Gln Lys Asn Gly Lys Leu Pro Pro Ala Asp Leu Lys Met Leu
305 310 315 320

Ser Leu Glu Glu Asp Val Thr Glu Lys Leu Ser Pro Ser Phe Ala Asp
325 330 335

Leu Phe Arg Thr Pro Arg Leu Arg Lys Arg Thr Phe Ile Leu Met Tyr
340 345 350

Leu Trp Phe Thr Asp Ser Val Leu Tyr Gln Gly Leu Ile Leu His Met
355 360 365

Gly Ala Thr Ser Gly Asn Leu Tyr Leu Asp Phe Leu Tyr Ser Ala Leu
370 375 380

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Gly Asn Trp Pro Ile Pro Gly Glu Arg Ile Pro Asp Val Ala Ala Leu
      35              40              45
Ser Met Gly Phe Ser Val Lys Glu Asp Leu Ser Trp Pro Gly Leu Ala
      50              55              60
Val Gly Asn Leu Phe His Arg Pro Arg Ala Thr Val Met Val Met Val
      65              70              75              80
Lys Gly Val Asn Lys Leu Ala Leu Pro Pro Gly Ser Val Ile Ser Tyr
      85              90              95

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Pro Leu Glu Asn Ala Val Pro Phe Ser Leu Asp Ser Val Ala Asn Ser
100 105 110

Ile His Ser Leu Phe Ser Glu Glu Thr Pro Val Val Leu Gln Leu Ala
115 120 125

Pro Ser Glu Glu Arg Val Tyr Met Val Gly Lys Ala Asn Ser Val Phe
130 135 140

Glu Asp Leu Ser Val Thr Leu Arg Gln Leu Arg Asn Arg Leu Phe Gln
145 150 155 160

Glu Asn Ser Val Leu Ser Ser Leu Pro Leu Asn Ser Leu Ser Arg Asn
165 170 175

Asn Glu Val Asp Leu Leu Phe Leu Ser Glu Leu Gln Val Leu His Asp
180 185 190

Ile Ser Ser Leu Leu Ser Arg His Lys His Leu Ala Lys Asp His Ser
195 200 205

Pro Asp Leu Tyr Ser Leu Glu Leu Ala Gly Leu Asp Glu Ile Gly Lys
210 215 220

Arg Tyr Gly Glu Asp Ser Glu Gln Phe Arg Asp Ala Ser Lys Ile Leu
225 230 235 240

Val Asp Ala Leu Gln Lys Phe Ala Asp Asp Met Tyr Ser Leu Tyr Gly
245 250 255

Gly Asn Ala Val Val Glu Leu Val Thr Val Lys Ser Phe Asp Thr Ser
260 265 270

Leu Ile Arg Lys Thr Arg Thr Ile Leu Glu Ala Lys Gln Ala Lys Asn
275 280 285

Pro Ala Ser Pro Tyr Asn Leu Ala Tyr Lys Tyr Asn Phe Glu Tyr Ser
290 295 300

Val Val Phe Asn Met Val Leu Trp Ile Met Ile Ala Leu Ala Leu Ala
305 310 315 320

Val Ile Ile Thr Ser Tyr Asn Ile Trp Asn Met Asp Pro Gly Tyr Asp
325 330 335

Ser Ile Ile Tyr Arg Met Thr Asn Gln Lys Ile Arg Met Asp
340 345 350

<210> 7

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<213> Homo sapiens

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Asn Val Ala Leu Leu Leu Pro Asn Trp Asp Val Thr Tyr Leu Leu Arg
35 40 45
Gly Leu Leu Gly Arg His Ala Met Leu Gly Thr Gly Leu Trp Gly Gly
50 55 60
Gly Leu Met Val Leu Thr Ala Ala Ile Leu Ile Ser Leu Met Gly Trp
65 70 75 80
Arg Tyr Gly Cys Phe Ser Lys Ser Gly Leu Cys Arg Ser Val Leu Thr
85 90 95
Ala Leu Leu Ser Gly Gly Leu Ala Leu Leu Gly Ala Leu Ile Cys Phe
100 105 110
Val Thr Ser Gly Val Ala Leu Lys Asp Gly Pro Phe Cys Met Phe Asp
115 120 125
Val Ser Ser Phe Asn Gln Thr Gln Ala Trp Lys Tyr Gly Tyr Pro Phe
130 135 140
Lys Asp Leu His Ser Arg Asn Tyr Leu Tyr Asp Arg Ser Leu Trp Asn
145 150 155 160
Ser Val Cys Leu Glu Pro Ser Ala Ala Val Val Trp His Val Ser Leu
165 170 175
Phe Ser Ala Leu Leu Cys Ile Ser Leu Leu Gln Leu Leu Val Val
180 185 190
Val His Val Ile Asn Ser Leu Leu Gly Leu Phe Cys Ser Leu Cys Glu
195 200 205
Lys

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20 25 30
Phe Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala Gly Lys Arg Pro
35 40 45
Pro Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro Glu Pro Glu Asp Glu

50 55 60
Asn Leu Tyr Glu Lys Asn Pro Asp Ser His Gly Tyr Asp Lys Asp Pro
65 70 75 80
Val Leu Asp Val Trp Asn Met Arg Leu Val Phe Phe Phe Gly Val Ser
85 90 95
Ile Ile Leu Val Leu Gly Ser Thr Phe Val Ala Tyr Leu Pro Asp Tyr
100 105 110
Arg Cys Thr Gly Cys Pro Arg Ala Trp Asp Gly Met Lys Glu Trp Ser
115 120 125
Arg Arg Glu Ala Glu Arg Leu Val Lys Tyr Arg Glu Ala Asn Gly Leu
130 135 140
Pro Ile Met Glu Ser Asn Cys Phe Asp Pro Ser Lys Ile Gln Leu Pro
145 150 155 160
Glu Asp Glu

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<212> PRT
<213> Homo sapiens

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20 25 30
Ser Cys Gln Glu Val Leu Trp Pro Leu Pro Ala Tyr Leu Leu Val Ser
35 40 45
Ala Gly Cys Tyr Ala Leu Gly Thr Val Gly Tyr Arg Val Ala Thr Phe
50 55 60
His Asp Cys Glu Asp Ala Ala Arg Glu Leu Gln Ser Gln Ile Gln Glu
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Ala Arg Ala Asp Leu Ala Arg Arg Gly Leu Arg Phe
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Ala Cys Gly Met Cys Leu Gly Trp Ser Leu Arg Val Cys Phe Gly Met
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Leu Pro Lys Ser Lys Thr Ser Lys Thr His Thr Asp Thr Glu Ser Glu
35 40 45

Ala Ser Ile Leu Gly Asp Ser Gly Glu Tyr Lys Met Ile Leu Val Val
50 55 60

Arg Asn Asp Leu Lys Met Gly Lys Gly Lys Val Ala Ala Gln Cys Ser
65 70 75 80

His Ala Ala Val Ser Ala Tyr Lys Gln Ile Gln Arg Arg Asn Pro Glu
85 90 95

Met Leu Lys Gln Trp Glu Tyr Cys Gly Gln Pro Lys Val Val Val Lys
100 105 110

Ala Pro Asp Glu Glu Thr Leu Ile Ala Leu Leu Ala His Ala Lys Met
115 120 125

Leu Gly Leu Thr Val Ser Leu Ile Gln Asp Ala Gly Arg Thr Gln Ile
130 135 140

Ala Pro Gly Ser Gln Thr Val Leu Gly Ile Gly Pro Gly Pro Ala Asp
145 150 155 160

Leu Ile Asp Lys Val Thr Gly His Leu Lys Leu Tyr
165 170

<210> 11
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<213> Homo sapiens

<400> 11
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Thr Thr Asn Ile Ile Thr Leu Ile Val Lys Leu Thr Arg Asp Ser Gln
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Ser Leu Cys Pro Tyr Asp Trp Ile Gly Phe Gln Asn Lys Cys Tyr Tyr
35 40 45

Phe Ser Lys Glu Glu Gly Asp Trp Asn Ser Ser Lys Tyr Asn Cys Ser
50 55 60

Thr Gln His Ala Asp Leu Thr Ile Ile Asp Asn Ile Glu Glu Met Asn
65 70 75 80

Phe Leu Arg Arg Tyr Lys Cys Ser Ser Asp His Trp Ile Gly Leu Lys
85 90 95

Met Ala Lys Asn Arg Thr Gly Gln Trp Val Asp Gly Ala Thr Phe Thr

100 105 110
Lys Ser Phe Gly Met Arg Gly Ser Glu Gly Cys Ala Tyr Leu Ser Asp
115 120 125
Asp Gly Ala Ala Thr Ala Arg Cys Tyr Thr Glu Arg Lys Trp Ile Cys
130 135 140
Arg Lys Arg Ile His
145

<210> 12
<211> 188
<212> PRT
<213> Homo sapiens

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Cys Thr Ala Leu Leu Ala Glu Gly Ile Thr Trp Val Leu Val Tyr Arg
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Thr Asp Lys Tyr Lys Arg Leu Lys Ala Glu Val Glu Lys Gln Ser Lys
35 40 45
Lys Leu Glu Lys Lys Lys Glu Thr Ile Thr Glu Ser Ala Gly Arg Gln
50 55 60
Gln Lys Lys Lys Ile Glu Arg Gln Glu Glu Lys Leu Lys Asn Asn Asn
65 70 75 80
Arg Asp Leu Ser Met Val Arg Met Lys Ser Met Phe Ala Ile Gly Phe
85 90 95
Cys Phe Thr Ala Leu Met Gly Met Phe Asn Ser Ile Phe Asp Gly Arg
100 105 110
Val Val Ala Lys Leu Pro Phe Thr Pro Leu Ser Tyr Ile Gln Gly Leu
115 120 125
Ser His Arg Asn Leu Leu Gly Asp Asp Thr Thr Asp Cys Ser Phe Ile
130 135 140
Phe Leu Tyr Ile Leu Cys Thr Met Ser Ile Arg Gln Asn Ile Gln Lys
145 150 155 160
Ile Leu Gly Leu Ala Pro Ser Arg Ala Ala Thr Lys Gln Ala Gly Gly
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Phe Leu Gly Pro Pro Pro Pro Ser Gly Lys Phe Ser
180 185

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Tyr Gln Ser Gln Ala Lys Gln Leu Phe Arg Lys Leu Asn Glu Gln Ser
35 40 45
Pro Thr Arg Cys Thr Leu Glu Ala Gly Ala Met Thr Phe His Tyr Ile
50 55 60
Ile Glu Gln Gly Val Cys Tyr Leu Val Leu Cys Glu Ala Ala Phe Pro
65 70 75 80
Lys Lys Leu Ala Phe Ala Tyr Leu Glu Asp Leu His Ser Glu Phe Asp
85 90 95
Glu Gln His Gly Lys Lys Val Pro Thr Val Ser Arg Pro Tyr Ser Phe
100 105 110
Ile Glu Phe Asp Thr Phe Ile Gln Lys Thr Lys Lys Leu Tyr Ile Asp
115 120 125
Ser Arg Ala Arg Arg Asn Leu Gly Ser Ile Asn Thr Glu Leu Gln Asp
130 135 140
Val Gln Arg Ile Met Val Ala Asn Ile Glu Glu Val Leu Gln Arg Gly
145 150 155 160
Glu Ala Leu Ser Ala Leu Asp Ser Lys Ala Asn Asn Leu Ser Ser Leu
165 170 175
Ser Lys Lys Tyr Arg Gln Asp Ala Lys Tyr Leu Asn Met Arg Ser Thr
180 185 190
Tyr Ala Lys Leu Ala Ala Val Ala Val Phe Phe Ile Met Leu Ile Val
195 200 205
Tyr Val Arg Phe Trp Trp Leu
210 215

<210> 14
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35 40 45
Gly Leu Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val Trp Val
50 55 60
Phe Leu Ala Thr Ser Gly Thr Leu Ala Gly Ile Met Gly Met Arg Phe
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Tyr His Ser Gly Lys Phe Met Pro Ala Gly Leu Ile Ala Gly Ala Ser
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Leu Leu Met Val Ala Lys Val Gly Val Ser Met Phe Asn Arg Pro His
100 105 110

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Gly Tyr Thr Ala Leu Val Val Ser Gly Gly Ile Val Gly Tyr Val Lys
20 25 30
Thr Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu
35 40 45
Ala Gly Leu Gly Ala Tyr Gln Leu Tyr Gln Asp Pro Arg Asn Val Trp
50 55 60
Gly Phe Leu Ala Ala Thr Ser Val Thr Phe Val Gly Val Met Gly Met
65 70 75 80
Arg Ser Tyr Tyr Tyr Gly Lys Phe Met Pro Val Gly Leu Ile Ala Gly
85 90 95
Ala Ser Leu Leu Met Ala Ala Lys Val Gly Val Arg Met Leu Met Thr
100 105 110
Ser Asp

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Cys Gly Val Thr Gly Ser Val Ser Val Ala Leu His Pro Leu Val Ile
35 40 45
Leu Asn Ile Ser Asp His Trp Ile Arg Met Arg Ser Gln Glu Gly Arg
50 55 60
Pro Val Gln Val Ile Gly Ala Leu Ile Gly Lys Gln Glu Gly Arg Asn
65 70 75 80
Ile Glu Val Met Asn Ser Phe Glu Leu Leu Ser His Thr Val Glu Glu
85 90 95
Lys Ile Ile Ile Asp Lys Glu Tyr Tyr Tyr Thr Lys Glu Glu Gln Phe
100 105 110
Lys Gln Val Phe Lys Glu Leu Glu Phe Leu Gly Trp Tyr Thr Thr Gly
115 120 125
Gly Pro Pro Asp Pro Ser Asp Ile His Val His Lys Gln Val Cys Glu
130 135 140
Ile Ile Glu Ser Pro Leu Phe Leu Lys Leu Asn Pro Met Thr Lys His
145 150 155 160
Thr Asp Leu Pro Val Ser Val Phe Glu Ser Val Ile Asp Ile Ile Asn
165 170 175
Gly Glu Ala Thr Met Leu Phe Ala Glu Leu Thr Tyr Thr Leu Ala Thr
180 185 190
Glu Glu Ala Glu Arg Ile Gly Val Asp His Val Ala Arg Met Thr Ala
195 200 205
Thr Gly Ser Gly Glu Asn Ser Thr Val Ala Glu His Leu Ile Ala Gln
210 215 220
His Ser Ala Ile Lys Met Leu His Ser Arg Val Lys Leu Ile Leu Glu
225 230 235 240
Tyr Val Lys Ala Ser Glu Ala Gly Glu Val Pro Phe Asn His Glu Ile
245 250 255
Leu Arg Glu Ala Tyr Ala Leu Cys His Cys Leu Pro Val Leu Ser Thr
260 265 270
Asp Lys Phe Lys Thr Asp Phe Tyr Asp Gln Cys Asn Asp Val Gly Leu
275 280 285
Met Ala Tyr Leu Gly Thr Ile Thr Lys Thr Cys Asn Thr Met Asn Gln
290 295 300

Phe Val Asn Lys Phe Asn Val Leu Tyr Asp Arg Gln Gly Ile Gly Arg
305 310 315 320

Arg Met Arg Gly Leu Phe Phe
325

<210> 17
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<400> 17
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Leu Val Ala Ile Leu Leu Val Phe Leu Ile Thr Ala Ile Leu Val Lys
35 40 45

Val Gln Leu Asp Ala Leu Pro Phe Phe Val Ile Thr Met Ile Lys Ile
50 55 60

Val Leu Ile Asn Ser Phe Gly Ala Ile Leu Gln Gly Ser Leu Phe Gly
65 70 75 80

Leu Ala Gly Leu Leu Pro Ala Ser Tyr Thr Ala Pro Ile Met Ser Gly
85 90 95

Gln Gly Leu Ala Gly Phe Phe Ala Ser Val Ala Met Ile Cys Ala Ile
100 105 110

Ala Ser Gly Ser Glu Leu Ser Glu Ser Ala Phe Gly Tyr Phe Ile Thr
115 120 125

Ala Cys Ala Val Ile Ile Leu Thr Ile Ile Cys Tyr Leu Gly Leu Pro
130 135 140

Arg Leu Glu Phe Tyr Arg Tyr Tyr Gln Gln Leu Lys Leu Glu Gly Pro
145 150 155 160

Gly Glu Gln Glu Thr Lys Leu Asp Leu Ile Ser Lys Gly Glu Glu Pro
165 170 175

Arg Ala Gly Lys Glu Glu Ser Gly Val Ser Val Ser Asn Ser Gln Pro
180 185 190

Thr Asn Glu Ser His Ser Ile Lys Ala Ile Leu Lys Asn Ile Ser Val
195 200 205

Leu Ala Phe Ser Val Cys Phe Ile Phe Thr Ile Thr Ile Gly Met Phe
210 215 220

Pro Ala Val Thr Val Glu Val Lys Ser Ser Ile Ala Gly Ser Ser Thr

225 230 235 240

Trp Glu Arg Tyr Phe Ile Pro Val Ser Cys Phe Leu Thr Phe Asn Ile
 245 250 255

Phe Asp Trp Leu Gly Arg Ser Leu Thr Ala Val Phe Met Trp Pro Gly
 260 265 270

Lys Asp Ser Arg Trp Leu Pro Ser Leu Val Leu Ala Arg Leu Val Phe
 275 280 285

Val Pro Leu Leu Leu Leu Cys Asn Ile Lys Pro Arg Arg Tyr Leu Thr
 290 295 300

Val Val Phe Glu His Asp Ala Trp Phe Ile Phe Phe Met Ala Ala Phe
305 310 315 320

Ala Phe Ser Asn Gly Tyr Leu Ala Ser Leu Cys Met Cys Phe Gly Pro
 325 330 335

Lys Lys Val Lys Pro Ala Glu Ala Glu Thr Ala Gly Ala Ile Met Ala
 340 345 350

Phe Phe Leu Cys Leu Gly Leu Ala Leu Gly Ala Val Phe Ser Phe Leu
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Phe Arg Ala Ile Val
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<210> 18
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<400> 18
Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
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Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile
 20 25 30

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
 35 40 45

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
 50 55 60

Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
 65 70 75 80

Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
 85 90 95

Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
 100 105 110

Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
115 120 125

Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser
130 135 140

Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
145 150 155 160

Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
165 170 175

Asp Arg His Lys Met Leu Ser
180

<210> 19
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<212> PRT
<213> Homo sapiens

<400> 19
Met Ala Ser Thr Val Val Ala Val Gly Leu Thr Ile Ala Ala Gly
1 5 10 15

Phe Ala Gly Arg Tyr Val Leu Gln Ala Met Lys His Met Glu Pro Gln
20 25 30

Val Lys Gln Val Phe Gln Ser Leu Pro Lys Ser Ala Phe Ser Gly Gly
35 40 45

Tyr Tyr Arg Gly Gly Phe Glu Pro Lys Met Thr Lys Arg Glu Ala Ala
50 55 60

Leu Ile Leu Gly Val Ser Pro Thr Ala Asn Lys Gly Lys Ile Arg Asp
65 70 75 80

Ala His Arg Arg Ile Met Leu Leu Asn His Pro Asp Lys Gly Gly Ser
85 90 95

Pro Tyr Ile Ala Ala Lys Ile Asn Glu Ala Lys Asp Leu Leu Glu Gly
100 105 110

Gln Ala Lys Lys
115

<210> 20
<211> 152
<212> PRT
<213> Homo sapiens

<400> 20
Met Ala Val Leu Ser Lys Glu Tyr Gly Phe Val Leu Leu Thr Gly Ala
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Ala Ser Phe Ile Met Val Ala His Leu Ala Ile Asn Val Ser Lys Ala

20 25 30

Arg Lys Lys Tyr Lys Val Glu Tyr Pro Ile Met Tyr Ser Thr Asp Pro
35 40 45

Glu Asn Gly His Ile Phe Asn Cys Ile Gln Arg Ala His Gln Asn Thr
50 55 60

Leu Glu Val Tyr Pro Pro Phe Leu Phe Phe Leu Ala Val Gly Gly Val
65 70 75 80

Tyr His Pro Arg Ile Ala Ser Gly Leu Gly Leu Ala Trp Ile Val Gly
85 90 95

Arg Val Leu Tyr Ala Tyr Gly Tyr Tyr Thr Gly Glu Pro Ser Lys Arg
100 105 110

Ser Arg Gly Ala Leu Gly Ser Ile Ala Leu Leu Gly Leu Val Gly Thr
115 120 125

Thr Val Cys Ser Ala Phe Gln His Leu Gly Trp Val Lys Ser Gly Leu
130 135 140

Gly Ser Gly Pro Lys Cys Cys His
145 150

<210> 21
<211> 559
<212> PRT
<213> Homo sapiens

<400> 21

Met Ala Pro Thr Leu Gln Gln Ala Tyr Arg Arg Arg Trp Trp Met Ala
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Cys Thr Ala Val Leu Glu Asn Leu Phe Phe Ser Ala Val Leu Leu Gly
20 25 30

Trp Gly Ser Leu Leu Ile Ile Leu Lys Asn Glu Gly Phe Tyr Ser Ser
35 40 45

Thr Cys Pro Ala Glu Ser Ser Thr Asn Thr Thr Gln Asp Glu Gln Arg
50 55 60

Arg Trp Pro Gly Cys Asp Gln Gln Asp Glu Met Leu Asn Leu Gly Phe
65 70 75 80

Thr Ile Gly Ser Phe Val Leu Ser Ala Thr Thr Leu Pro Leu Gly Ile
85 90 95

Leu Met Asp Arg Phe Gly Pro Arg Pro Val Arg Leu Val Gly Ser Ala
100 105 110

Cys Phe Thr Ala Ser Cys Thr Leu Met Ala Leu Ala Ser Arg Asp Val
115 120 125

Glu Ala Leu Ser Pro Leu Ile Phe Leu Ala Leu Ser Leu Asn Gly Phe
130 135 140

Gly Gly Ile Cys Leu Thr Phe Thr Ser Leu Thr Leu Pro Asn Met Phe
145 150 155 160

Gly Asn Leu Arg Ser Thr Leu Met Ala Leu Met Ile Gly Ser Tyr Ala
165 170 175

Ser Ser Ala Ile Thr Phe Pro Gly Ile Lys Leu Ile Tyr Asp Ala Gly
180 185 190

Val Ala Phe Val Val Ile Met Phe Thr Trp Ser Gly Leu Ala Cys Leu
195 200 205

Ile Phe Leu Asn Cys Thr Leu Asn Trp Pro Ile Glu Ala Phe Pro Ala
210 215 220

Pro Glu Glu Val Asn Tyr Thr Lys Lys Ile Lys Leu Ser Gly Leu Ala
225 230 235 240

Leu Asp His Lys Val Thr Gly Asp Leu Phe Tyr Thr His Val Thr Thr
245 250 255

Met Gly Gln Arg Leu Ser Gln Lys Ala Pro Ser Leu Glu Asp Gly Ser
260 265 270

Asp Ala Phe Met Ser Pro Gln Asp Val Arg Gly Thr Ser Glu Asn Leu
275 280 285

Pro Glu Arg Ser Val Pro Leu Arg Lys Ser Leu Cys Ser Pro Thr Phe
290 295 300

Leu Trp Ser Leu Leu Thr Met Gly Met Thr Gln Leu Arg Ile Ile Phe
305 310 315 320

Tyr Met Ala Ala Val Asn Lys Met Leu Glu Tyr Leu Val Thr Gly Gly
325 330 335

Gln Glu His Glu Thr Asn Glu Gln Gln Gln Lys Val Ala Glu Thr Val
340 345 350

Gly Phe Tyr Ser Ser Val Phe Gly Ala Met Gln Leu Leu Cys Leu Leu
355 360 365

Thr Cys Pro Leu Ile Gly Tyr Ile Met Asp Trp Arg Ile Lys Asp Cys
370 375 380

Val Asp Ala Pro Thr Gln Gly Thr Val Leu Gly Asp Ala Arg Asp Gly
385 390 395 400

Val Ala Thr Lys Ser Ile Arg Pro Arg Tyr Cys Lys Ile Gln Lys Leu
405 410 415

Thr Asn Ala Ile Ser Ala Phe Thr Leu Thr Asn Leu Leu Leu Val Gly
420 425 430

Phe Gly Ile Thr Cys Leu Ile Asn Asn Leu His Leu Gln Phe Val Thr
435 440 445

Phe Val Leu His Thr Ile Val Arg Gly Phe Phe His Ser Ala Cys Gly
450 455 460

Ser Leu Tyr Ala Ala Val Phe Pro Ser Asn His Phe Gly Thr Leu Thr
465 470 475 480

Gly Leu Gln Ser Leu Ile Ser Ala Val Phe Ala Leu Leu Gln Gln Pro
485 490 495

Leu Phe Met Ala Met Val Gly Pro Leu Lys Gly Glu Pro Phe Trp Val
500 505 510

Asn Leu Gly Leu Leu Leu Phe Ser Leu Leu Gly Phe Leu Leu Pro Ser
515 520 525

Tyr Leu Phe Tyr Tyr Arg Ala Arg Leu Gln Gln Glu Tyr Ala Ala Asn
530 535 540

Gly Met Gly Pro Leu Lys Val Leu Ser Gly Ser Glu Val Thr Ala
545 550 555

<210> 22
<211> 330
<212> PRT
<213> Homo sapiens

<400> 22
Met Glu Gly Ala Pro Pro Gly Ser Leu Ala Leu Arg Leu Leu Phe
1 5 10 15

Val Ala Leu Pro Ala Ser Gly Trp Leu Thr Thr Gly Ala Pro Glu Pro
20 25 30

Pro Pro Leu Ser Gly Ala Pro Gln Asp Gly Ile Arg Ile Asn Val Thr
35 40 45

Thr Leu Lys Asp Asp Gly Asp Ile Ser Lys Gln Gln Val Val Leu Asn
50 55 60

Ile Thr Tyr Glu Ser Gly Gln Val Tyr Val Asn Asp Leu Pro Val Asn
65 70 75 80

Ser Gly Val Thr Arg Ile Ser Cys Gln Thr Leu Ile Val Lys Asn Glu
85 90 95

Asn Leu Glu Asn Leu Glu Glu Lys Glu Tyr Phe Gly Ile Val Ser Val
100 105 110

Arg Ile Leu Val His Glu Trp Pro Met Thr Ser Gly Ser Ser Leu Gln
115 120 125

Leu Ile Val Ile Gln Glu Glu Val Val Glu Ile Asp Gly Lys Gln Val
130 135 140

Gln Gln Lys Asp Val Thr Glu Ile Asp Ile Leu Val Lys Asn Arg Gly
145 150 155 160
Val Leu Arg His Ser Asn Tyr Thr Leu Pro Leu Glu Glu Ser Met Leu
165 170 175
Tyr Ser Ile Ser Arg Asp Ser Asp Ile Leu Phe Thr Leu Pro Asn Leu
180 185 190
Ser Lys Lys Glu Ser Val Ser Ser Leu Gln Thr Thr Ser Gln Tyr Leu
195 200 205
Ile Arg Asn Val Glu Thr Thr Val Asp Glu Asp Val Leu Pro Gly Lys
210 215 220
Leu Pro Glu Thr Pro Leu Arg Ala Glu Pro Pro Ser Ser Tyr Lys Val
225 230 235 240
Met Cys Gln Trp Met Glu Lys Phe Arg Lys Asp Leu Cys Arg Phe Trp
245 250 255
Ser Asn Val Phe Pro Val Phe Phe Gln Phe Leu Asn Ile Met Val Val
260 265 270
Gly Ile Thr Gly Ala Ala Val Val Ile Thr Ile Leu Lys Val Phe Phe
275 280 285
Pro Val Ser Glu Tyr Lys Gly Ile Leu Gln Leu Asp Lys Val Asp Val
290 295 300
Ile Pro Val Thr Ala Ile Asn Leu Tyr Pro Asp Gly Pro Glu Lys Arg
305 310 315 320
Ala Glu Asn Leu Glu Asp Lys Thr Cys Ile
325 330

<210> 23
<211> 108
<212> PRT
<213> Homo sapiens

<400> 23
Met Ser Leu Thr Ser Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala
1 5 10 15
Val Thr Ile Ala Ala Gly Thr Ala Ala Ile Gly Tyr Leu Ala Tyr Lys
20 25 30
Arg Phe Tyr Val Lys Asp His Arg Asn Lys Ala Met Ile Asn Leu His
35 40 45
Ile Gln Lys Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp
50 55 60
Leu Gly Asp Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe

70

80

Pro Phe Cys Asp Gly Ala His Thr Lys His Asn Glu Glu Thr Gly Asp
85 90 95

Asn Val Gly Pro Leu Ile Ile Lys Lys Lys Glu Thr
100 105

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<210> 24
<211> 101
<212> PRT
<213> Homo sapiens
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<400> 24
Met Asn Leu Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg
1 5 10 15

Lys Tyr Tyr Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp Leu Val
20 25 30

Asn Ile Phe Trp Phe Phe Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr
35 40 45

Glu Gln Ser Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe
50 55 60

Leu Phe Trp Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile
65 70 75 80

Tyr Arg Pro Arg Trp Gly Ala Leu Gly Asp Tyr Leu Ser Phe Thr Ile
85 90 95

Pro Leu Gly Thr Pro
100

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<210> 25
<211> 372
<212> PRT
<213> Homo sapiens
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<400> 25
Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala
1 5 10 15

Ile Gly Ala Phe Thr Leu Leu Leu Phe Ser Leu Leu Val Ser Pro Pro
20 25 30

Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala
35 40 45

Trp Pro Thr Pro Pro Thr Arg Pro Ala Pro Ala Pro Cys His Ala Asn
50 55 60

Thr Ser Met Val Thr His Pro Asp Phe Ala Thr Gln Pro Gln His Val
65 70 75 80

Gln Asn Phe Leu Leu Tyr Arg His Cys Arg His Phe Pro Leu Leu Gln
85 90 95

Asp Val Pro Pro Ser Lys Cys Ala Gln Pro Val Phe Leu Leu Val
100 105 110

Ile Lys Ser Ser Pro Ser Asn Tyr Val Arg Arg Glu Leu Leu Arg Arg
115 120 125

Thr Trp Gly Arg Glu Arg Lys Val Arg Gly Leu Gln Leu Arg Leu Leu
130 135 140

Phe Leu Val Gly Thr Ala Ser Asn Pro His Glu Ala Arg Lys Val Asn
145 150 155 160

Arg Leu Leu Glu Leu Glu Ala Gln Thr His Gly Asp Ile Leu Gln Trp
165 170 175

Asp Phe His Asp Ser Phe Phe Asn Leu Thr Leu Lys Gln Val Leu Phe
180 185 190

Leu Gln Trp Gln Glu Thr Arg Cys Ala Asn Ala Ser Phe Val Leu Asn
195 200 205

Gly Asp Asp Asp Val Phe Ala His Thr Asp Asn Met Val Phe Tyr Leu
210 215 220

Gln Asp His Asp Pro Gly Arg His Leu Phe Val Gly Gln Leu Ile Gln
225 230 235 240

Asn Val Gly Pro Ile Arg Ala Phe Trp Ser Lys Tyr Tyr Val Pro Glu
245 250 255

Val Val Thr Gln Asn Glu Arg Tyr Pro Pro Tyr Cys Gly Gly Gly Gly
260 265 270

Phe Leu Leu Ser Arg Phe Thr Ala Ala Ala Leu Arg Arg Ala Ala His
275 280 285

Val Leu Asp Ile Phe Pro Ile Asp Asp Val Phe Leu Gly Met Cys Leu
290 295 300

Glu Leu Glu Gly Leu Lys Pro Ala Ser His Ser Gly Ile Arg Thr Ser
305 310 315 320

Gly Val Arg Ala Pro Ser Gln His Leu Ser Ser Phe Asp Pro Cys Phe
325 330 335

Tyr Arg Asp Leu Leu Leu Val His Arg Phe Leu Pro Tyr Glu Met Leu
340 345 350

Leu Met Trp Asp Ala Leu Asn Gln Pro Asn Leu Thr Cys Gly Asn Gln
355 360 365

Thr Gln Ile Tyr
370

<210> 26
<211> 615
<212> DNA
<213> Homo sapiens

<400> 26
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ctgacggaga cttcgccctt catgtggtcc aacctgggca ttggcctagc tatctccctg 180
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<210> 27
<211> 1113
<212> DNA
<213> Homo sapiens

<400> 27
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ccttaccac agccccctt ccagccctcc ccctacggtc agccagggtta ccccatggc 180
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caggggccct accacaaga gggctaccca caggggccct accccaagg gggctacccc 300
caggggccat atccccagag ccccttcccc cccaaccct atggacagcc acaggtcttc 360
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tactatgaca accaggactt ccctgccacc aactgggatg acaagagcat ccgacaggcc 480
ttcatccgca aggtgttcct agtgtgacc ttgcagctgt cggtgaccct gtccacgggtg 540
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tacatcctca ccatcattgg ccgcgccaaag gag 1113

<210> 28
<211> 537
<212> DNA
<213> Homo sapiens

<400> 28
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agagccaggg gatgtgttcc ttatattgga attgtgacga tcctcatgaa tgactatcct 480
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<210> 29
<211> 1041
<212> DNA
<213> Homo sapiens

<400> 29
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<210> 30
<211> 1662
<212> DNA
<213> Homo sapiens

<400> 30
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gtgttggggc tgcttgccgc gggagtgcg ctacttcttc cagagaccaa gggggtcgct 1560
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acgatttacc ttaaggtcca aacctcagaa ccctcgggca cc 1662

<210> 31
<211> 1050
<212> DNA
<213> Homo sapiens

<400> 31
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atattaaaat caccagggtc tgttgttttc cgaaatggaa attggcctat accaggagag 120
cggatcccag acgtggctgc attgtccatg ggcttctctg tgaaagaaga ctttcttgg 180
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aggatgacaa accagaagat tcgaatggat 1050

<210> 32
<211> 627
<212> DNA
<213> Homo sapiens

<400> 32
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ggttaccat tcaaagacct gcatagtagg aattatctgt atgaccgttc gctctggaac 480
tccgtctgcc tggagccctc tgcagctgtt gtctggcacg tgcctcctt ctcgcccctt 540
ctgtgcatca gcctgtcca gcttctcctg gtggtcgttc atgtcatcaa cagcctcctg 600
ggccttttct gcagcctctg cgagaag 627

<210> 33
<211> 489
<212> DNA
<213> Homo sapiens

<400> 33

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tccgctgtgg cgggaaagcg gccccagaa ccgaccacac cgtggcaaga ggaccagaa 180
cccgaggacg aaaacttgta tgagaagaac ccagactccc atggttatga caaggacccc 240
gttttgacg tctggaacat gcgacttgct ttcttctttg gcgtctccat catcctggtc 300
cttggcagca cctttgtggc ctatctgcct gactacaggt gcacaggggtg tccaagagcg 360
tgggatggga tgaaagagtg gtcccggcg gaagctgaga ggcttgtaaa ataccgagag 420
gccaatggcc ttccatcat ggaatccaac tgcttcgacc ccagcaagat ccagctgcc 480
gaggatgag 489

<210> 34
<211> 276
<212> DNA
<213> Homo sapiens

<400> 34
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ctgcccgcct acttgctggt gtccgcccgc tgctatgcc tgggcaactgt gggctatcgt 180
gtggccactt ttcagtactg cgaggacgcc gcacgcgagc tgcaagacca gatacaggag 240
gcccagagccg acttagcccg cagggggctg cgcttc 276

<210> 35
<211> 516
<212> DNA
<213> Homo sapiens

<400> 35
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cgtactcaga ttgcaccagg ctctcaaaact gtcctaggga ttgggcccagg accagcagac 480

516

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<210> 36
<211> 447
<212> DNA
<213> Homo sapiens

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tacaactggt ccaactcaaca tgccgacctt actataattg acaacataga agaaatgaat 240
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cgaacaggac aatgggtaga tggagctaca ttaccaaat cgtttggcat gagagggagt 360
gaaggatgtg cctacctcag cgatgatggt gcagcaacag ctagatgtta caccgaaaga 420
aaatggattt gcaggaaaag aatacac 447

<210> 37
<211> 564
<212> DNA
<213> Homo sapiens

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<211> 645
<212> DNA

<213> Homo sapiens

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tttcgaaagt tgaatgaaca gtcccctacc agatgtacct tggaagcagg agccatgact 180
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<210> 39
<211> 336
<212> DNA
<213> Homo sapiens

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taccactctg gaaaattcat gcctgcagggt ttaattgcag gtgccagttt gctgatggtc 300
gccaaagttg gagttagtat gttcaacaga ccccat 336

<210> 40
<211> 342
<212> DNA
<213> Homo sapiens

<400> 40
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<210> 41
<211> 981
<212> DNA
<213> Homo sapiens

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<210> 42
<211> 1119
<212> DNA
<213> Homo sapiens

<400> 42
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ctgatcactg ccatectggt gaaggtgcag ctggatgctc tgcccttctt tgtcatcacc 180
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<210> 43
<211> 549
<212> DNA
<213> Homo sapiens

<400> 43
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gctgctgcat cctcggggg accccgagca aacacagtcc tggagcgtgt ggaaggtgcc 480

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<210> 44
<211> 348
<212> DNA
<213> Homo sapiens

<400> 44
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cggaagcag cattaatact aggtgtaagc cctactgcca ataaagggaa aataagagat 240
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gccaaaatca atgaagctaa agatttacta gaaggtcaag ctaaaaaa 348

<210> 45
<211> 456
<212> DNA
<213> Homo sapiens

<400> 45
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<210> 46
<211> 1677
<212> DNA
<213> Homo sapiens

<400> 46
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<210> 47
<211> 990
<212> DNA

<213> Homo sapiens

<400> 47

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ggaaaacaag ttcagcaaaa gtagtgcact gaaattgata ttttagttaa gaaccgggga 480
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<210> 48

<211> 324

<212> DNA

<213> Homo sapiens

<400> 48

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ctgatcatca agaaaaaaga aact 324

<210> 49
<211> 303
<212> DNA
<213> Homo sapiens

<400> 49
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ccc 303

<210> 50
<211> 1116
<212> DNA
<213> Homo sapiens

<400> 50
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<210> 51
<211> 986
<212> DNA
<213> Homo sapiens

<220>
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<222> (82)..(696)

<400> 51
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acccccgccg ccgtgcgcgc c atg acg ggg cta gca ctg ctc tac tcc ggg 111
Met Thr Gly Leu Ala Leu Leu Tyr Ser Gly
1 5 10

gtc ttc gtg gcc ttc tgg gcc tgc gcg ctg gcc gtg gga gtc tgc tac 159
Val Phe Val Ala Phe Trp Ala Cys Ala Leu Ala Val Gly Val Cys Tyr
15 20 25

acc att ttt gat ttg ggc ttc cgc ttt gat gtg gca tgg ttc ctg acg 207
Thr Ile Phe Asp Leu Gly Phe Arg Phe Asp Val Ala Trp Phe Leu Thr
30 35 40

gag act tcg ccc ttc atg tgg tcc aac ctg ggc att ggc cta gct atc 255
Glu Thr Ser Pro Phe Met Trp Ser Asn Leu Gly Ile Gly Leu Ala Ile
45 50 55

tcc ctg tct gtg gtt ggg gca gcc tgg ggc atc tat att acc ggc tcc 303
Ser Leu Ser Val Val Gly Ala Ala Trp Gly Ile Tyr Ile Thr Gly Ser
60 65 70

tcc atc att ggt gga gga gtg aag gcc ccc agg atc aag acc aag aac 351
Ser Ile Ile Gly Gly Val Lys Ala Pro Arg Ile Lys Thr Lys Asn
75 80 85 90

ctg gtc agc atc atc ttc tgt gag gct gtg gcc atc tac ggc atc atc 399
Leu Val Ser Ile Ile Phe Cys Glu Ala Val Ala Ile Tyr Gly Ile Ile
95 100 105

atg gca att gtc att agc aac atg gct gag cct ttc agt gcc aca gac 447
Met Ala Ile Val Ile Ser Asn Met Ala Glu Pro Phe Ser Ala Thr Asp
110 115 120

ccc aag gcc atc ggc cat cgg aac tac cat gca ggc tac tcc atg ttt 495
Pro Lys Ala Ile Gly His Arg Asn Tyr His Ala Gly Tyr Ser Met Phe
125 130 135

ggg gct ggc ctc acc gta ggc ctg tct aac ctc ttc tgt gga gtc tgc 543
Gly Ala Gly Leu Thr Val Gly Leu Ser Asn Leu Phe Cys Gly Val Cys

140 145 150

gtg ggc atc gtg ggc agt ggg gct gcc ctg gcc gat gct cag aac ccc 591
Val Gly Ile Val Gly Ser Gly Ala Ala Leu Ala Asp Ala Gln Asn Pro
155 160 165 170

agc ctc ttt gta aag att ctc atc gtg gag atc ttt ggc agc gcc att 639
Ser Leu Phe Val Lys Ile Leu Ile Val Glu Ile Phe Gly Ser Ala Ile
175 180 185

ggc ctc ttt ggg gtc atc gtc gca att ctt cag acc tcc aga gtg aag 687
Gly Leu Phe Gly Val Ile Val Ala Ile Leu Gln Thr Ser Arg Val Lys
190 195 200

atg ggt gac tagatgatat gtgtgggtgg ggccgtgcct cacttttatt 736
Met Gly Asp
205

tattgctggt tttcctggga cagctggagc tgtgtccctt agcctttcag aggcttggtg 796

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<210> 52
<211> 1824
<212> DNA
<213> Homo sapiens

<220>
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<222> (133)..(1245)

<400> 52

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gaacccgagg cc atg tcc cat gaa aag agt ttt ttg gtg tct ggg gac aac 171
Met Ser His Glu Lys Ser Phe Leu Val Ser Gly Asp Asn
1 5 10

tat cct ccc ccc aac cct gga tat ccg ggg ggg ccc cag cca ccc atg 219
Tyr Pro Pro Pro Asn Pro Gly Tyr Pro Gly Gly Pro Gln Pro Pro Met
15 20 25

ccc ccc tat gct cag cct ccc tac cct ggg gcc cct tac cca cag ccc 267
Pro Pro Tyr Ala Gln Pro Pro Tyr Pro Gly Ala Pro Tyr Pro Gln Pro
30 35 40 45

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Pro Phe Gln Pro Ser Pro Tyr Gly Gln Pro Gly Tyr Pro His Gly Pro

50	55	60	
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Ser Pro Tyr Pro Gln Gly Gly Tyr	Pro Gln Gly Pro Tyr	Pro Gln Gly	
65	70	75	
ggc tac cca cag ggc ccc tac cca caa gag ggc tac cca cag ggc ccc			411
Gly Tyr Pro Gln Gly Pro Tyr	Pro Gln Glu Gly Tyr	Pro Gln Gly Pro	
80	85	90	
tac ccc caa ggg ggc tac ccc cag ggg cca tat ccc cag agc ccc ttc			459
Tyr Pro Gln Gly Gly Tyr	Pro Gln Gly Pro Tyr	Pro Gln Ser Pro Phe	
95	100	105	
ccc ccc aac ccc tat gga cag cca cag gtc ttc cca gga caa gac cct			507
Pro Pro Asn Pro Tyr	Gly Gln Pro Gln Val Phe Pro Gly Gln Asp Pro		
110	115	120	125
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Asp Ser Pro Gln His Gly Asn Tyr	Gln Glu Glu Gly Pro Pro Ser Tyr		
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Tyr Asp Asn Gln Asp Phe Pro Ala	Thr Asn Trp Asp Asp Lys Ser Ile		
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cga cag gcc ttc atc cgc aag gtg ttc cta gtg ctg acc ttg cag ctg			651
Arg Gln Ala Phe Ile Arg Lys Val	Phe Leu Val Leu Thr Leu Gln Leu		
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tcg gtg acc ctg tcc acg gtg tct gtg ttc act ttt gtt gcg gag gtg			699
Ser Val Thr Leu Ser Thr Val Ser Val Phe Thr	Phe Val Ala Glu Val		
175	180	185	
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Lys Gly Phe Val Arg Glu Asn Val Trp Thr	Tyr Tyr Val Ser Tyr Ala		
190	195	200	205
gtc ttc ttc atc tct ctc atc gtc ctc agc tgt tgt ggg gac ttc cgg			795
Val Phe Phe Ile Ser Leu Ile Val Leu Ser Cys Cys Gly Asp Phe Arg			
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cga aag cac ccc tgg aac ctt gtt gca ctg tcg gtc ctg acc gcc agc			843
Arg Lys His Pro Trp Asn Leu Val	Ala Leu Ser Val Leu Thr Ala Ser		
225	230	235	
ctg tcg tac atg gtg ggg atg atc gcc agc ttc tac aac acc gag gca			891
Leu Ser Tyr Met Val Gly Met	Ile Ala Ser Phe Tyr Asn Thr Glu Ala		
240	245	250	
gtc atc atg gcc gtg ggc atc acc aca gcc gtc tgc ttc acc gtc gtc			939
Val Ile Met Ala Val Gly Ile Thr Thr Ala Val	Cys Phe Thr Val Val		
255	260	265	
atc ttc tcc atg cag acc cgc tac gac ttc acc tca tgc atg ggc gtg			987
Ile Phe Ser Met Gln Thr Arg Tyr Asp Phe	Thr Ser Cys Met Gly Val		
270	275	280	285

ctc ctg gtg agc atg gtg gtg ctc ttc atc ttc gcc att ctc tgc atc 1035
Leu Leu Val Ser Met Val Val Leu Phe Ile Phe Ala Ile Leu Cys Ile
290 295 300

ttc atc cgg aac cgc atc ctg gag atc gtg tac gcc tca ctg ggc gct 1083
Phe Ile Arg Asn Arg Ile Leu Glu Ile Val Tyr Ala Ser Leu Gly Ala
305 310 315

ctg ctc ttc acc tgc ttc ctc gca gtg gac acc cag ctg ctg ctg ggg 1131
Leu Leu Phe Thr Cys Phe Leu Ala Val Asp Thr Gln Leu Leu Leu Gly
320 325 330

aac aag cag ctg tcc ctg agc cca gaa gag tat gtg ttt gct gcg ctg 1179
Asn Lys Gln Leu Ser Leu Ser Pro Glu Glu Tyr Val Phe Ala Ala Leu
335 340 345

aac ctg tac aca gac atc atc aac atc ttc ctg tac atc ctc acc atc 1227
Asn Leu Tyr Thr Asp Ile Ile Asn Ile Phe Leu Tyr Ile Leu Thr Ile
350 355 360 365

att ggc cgc gcc aag gag tagccgagct ccagctcgct gtgcccgcctc 1275
Ile Gly Arg Ala Lys Glu
370

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cggagtgggg gtcttatccc tgtgtgagc cctgagggca gagaggatgg catgtttcag 1755

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Met Leu Ser Leu Asp Phe Leu Asp Asp Val Arg Arg Met Asn Lys Arg
1 5 10 15

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Gln Leu Tyr Tyr Gln Val Leu Asn Phe Gly Met Ile Val Ser Ser Ala
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Leu Met Ile Trp Lys Gly Leu Met Val Ile Thr Gly Ser Glu Ser Pro
35 40 45

att gta gtg gtg ctc agt ggc agc atg gaa cct gca ttt cat aga gga 253
Ile Val Val Val Leu Ser Gly Ser Met Glu Pro Ala Phe His Arg Gly
50 55 60

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Asp Leu Leu Phe Leu Thr Asn Arg Val Glu Asp Pro Ile Arg Val Gly
65 70 75 80

gaa att gtt gtt ttt agg ata gaa gga aga gag att cct ata gtt cac 349
Glu Ile Val Val Phe Arg Ile Glu Gly Arg Glu Ile Pro Ile Val His
85 90 95

cga gtc ttg aag att cat gaa aag caa aat ggg cat atc aag ttt ttg 397
Arg Val Leu Lys Ile His Glu Lys Gln Asn Gly His Ile Lys Phe Leu
100 105 110

acc aaa gga gat aat aat gcg gtt gat gac cga ggc ctc tat aaa caa 445
Thr Lys Gly Asp Asn Asn Ala Val Asp Asp Arg Gly Leu Tyr Lys Gln
115 120 125

gga caa cat tgg cta gag aaa aaa gat gtt gtg ggg aga gcc agg gga 493
Gly Gln His Trp Leu Glu Lys Lys Asp Val Val Gly Arg Ala Arg Gly
130 135 140

ttt gtt cct tat att gga att gtg acg atc ctc atg aat gac tat cct 541
Phe Val Pro Tyr Ile Gly Ile Val Thr Ile Leu Met Asn Asp Tyr Pro
145 150 155 160

aaa ttt aag tat gca gtt ctc ttt ttg ctg ggt tta ttc gtg ctg gtt 589
Lys Phe Lys Tyr Ala Val Leu Phe Leu Leu Gly Leu Phe Val Leu Val
165 170 175

cat cgt gag taagaagcct gccttgctgt tcctgggaag atgccatagt 638
His Arg Glu

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gtgttggtgc ttctgggtag cactggtttg cattagttta tgtttccatg ccagagtttg 758

tgtgggcggg cgcattgtgca ccacagagtg cactcgaggg gactttcagt cacaggattt 818

cataattgtc attgtcacac tttaaattt ttgtacatca gtgaattttt ttatattaaa 878

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tacagagact tgtaaatgaa aatgcagctc tgcacgagtt tgaaaccgtc atacctcctt 998
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Met Ala Leu Leu Phe
1 5

tcc ttg atc ctt gcc att tgc acc aga cct gga ttc cta gcg tct cca 164
Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly Phe Leu Ala Ser Pro
10 15 20

tct gga gtg cgg ctg gtg ggg ggc ctc cac cgc tgt gaa ggg cgg gtg 212
Ser Gly Val Arg Leu Val Gly Gly Leu His Arg Cys Glu Gly Arg Val
25 30 35

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Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val Cys Asp Asp Gly Trp
40 45 50

gac att aag gac gtg gct gtg ttg tgc cgg gag ctg ggc tgt gga gct 308
Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu Leu Gly Cys Gly Ala
55 60 65

gcc agc gga acc cct agt ggt att ttg tat gag cca cca gca gaa aaa 356
Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu Pro Pro Ala Glu Lys
70 75 80 85

gag caa aag gtc ctc atc caa tca gtc agt tgc aca gga aca gaa gat 404
Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys Thr Gly Thr Glu Asp
90 95 100

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Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr Asp Cys Ser His Glu
105 110 115

gaa gat gct ggg gca tcg tgt gag aac cca gag agc tct ttc tcc cca 500
Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu Ser Ser Phe Ser Pro
120 125 130

gtc cca gag ggt gtc agg ctg gct gac ggc cct ggg cat tgc aag gga 548

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Arg	Val	Glu	Val	Lys	His	Gln	Asn	Gln	Trp	Tyr	Thr	Val	Cys	Gln	Thr	
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ggc	tgg	agc	ctc	cgg	gcc	gca	aag	gtg	gtg	tgc	cgg	cag	ctg	gga	tgt	644
Gly	Trp	Ser	Leu	Arg	Ala	Ala	Lys	Val	Val	Cys	Arg	Gln	Leu	Gly	Cys	
					170				175					180		
ggg	agg	gct	gta	ctg	act	caa	aaa	cgc	tgc	aac	aag	cat	gcc	tat	ggc	692
Gly	Arg	Ala	Val	Leu	Thr	Gln	Lys	Arg	Cys	Asn	Lys	His	Ala	Tyr	Gly	
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cga	aaa	ccc	atc	tgg	ctg	agc	cag	atg	tca	tgc	tca	gga	cga	gaa	gca	740
Arg	Lys	Pro	Ile	Trp	Leu	Ser	Gln	Met	Ser	Cys	Ser	Gly	Arg	Glu	Ala	
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Thr	Leu	Gln	Asp	Cys	Pro	Ser	Gly	Pro	Trp	Gly	Lys	Asn	Thr	Cys	Asn	
		215				220				225						
cat	gat	gaa	gac	acg	tgg	gtc	gaa	tgt	gaa	gat	ccc	ttt	gac	ttg	aga	836
His	Asp	Glu	Asp	Thr	Trp	Val	Glu	Cys	Glu	Asp	Pro	Phe	Asp	Leu	Arg	
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Leu	Val	Gly	Gly	Asp	Asn	Leu	Cys	Ser	Gly	Arg	Leu	Glu	Val	Leu	His	
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Lys	Gly	Val	Trp	Gly	Ser	Val	Cys	Asp	Asp	Asn	Trp	Gly	Glu	Lys	Glu	
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gac	cag	gtg	gta	tgc	aag	caa	ctg	ggc	tgt	ggg	aag	tcc	ctc	tct	ccc	980
Asp	Gln	Val	Val	Cys	Lys	Gln	Leu	Gly	Cys	Gly	Lys	Ser	Leu	Ser	Pro	
		280				285						290				
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Ser	Phe	Arg	Asp	Arg	Lys	Cys	Tyr	Gly	Pro	Gly	Val	Gly	Arg	Ile	Trp	
		295				300					305					
ctg	gat	aat	gtt	cgt	tgc	tca	ggg	gag	gag	cag	tcc	ctg	gag	cag	tgc	1076
Leu	Asp	Asn	Val	Arg	Cys	Ser	Gly	Glu	Glu	Gln	Ser	Leu	Glu	Gln	Cys	
		310			315				320					325		
cag	cac	aga	ttt	tgg	ggg	ttt	cac	gac	tgc	acc	cac	cag	gaa	gat	gtg	1124
Gln	His	Arg	Phe	Trp	Gly	Phe	His	Asp	Cys	Thr	His	Gln	Glu	Asp	Val	
				330					335					340		
gct	gtc	atc	tgc	tca	gga	tagtatacctg	gtgttgcttg	acctggcccc								1172
Ala	Val	Ile	Cys	Ser	Gly											
				345												
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Met Pro Thr Val Asp Asp Ile Leu
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gag cag gtt ggg gag tct ggc tgg ttc cag aag caa gcc ttc ctc atc 161
Glu Gln Val Gly Glu Ser Gly Trp Phe Gln Lys Gln Ala Phe Leu Ile
10 15 20

tta tgc ctg ctg tgc gct gcc ttt gcg ccc atc tgt gtg ggc atc gtc 209
Leu Cys Leu Leu Ser Ala Ala Phe Ala Pro Ile Cys Val Gly Ile Val
25 30 35 40

ttc ctg ggt ttc aca cct gac cac cac tgc cag agt cct ggg gtg gct 257
Phe Leu Gly Phe Thr Pro Asp His His Cys Gln Ser Pro Gly Val Ala
45 50 55

gag ctg agc cag cgc tgt ggc tgg agc cct gcg gag gag ctg aac tat 305
Glu Leu Ser Gln Arg Cys Gly Trp Ser Pro Ala Glu Glu Leu Asn Tyr
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aca gtg cca ggc ctg ggg ccc gcg ggc gag gcc ttc ctt ggc cag tgc 353
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75 80 85

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Arg Arg Tyr Glu Val Asp Trp Asn Gln Ser Ala Leu Ser Cys Val Asp
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Pro Leu Ala Ser Leu Ala Thr Asn Arg Ser His Leu Pro Leu Gly Pro
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Cys Gln Asp Gly Trp Val Tyr Asp Thr Pro Gly Ser Ser Ile Val Thr	
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Glu Phe Asn Leu Val Cys Ala Asp Ser Trp Lys Leu Asp Leu Phe Gln	
140 145 150	
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Ser Cys Leu Asn Ala Gly Phe Phe Phe Gly Ser Leu Gly Val Gly Tyr	
155 160 165	
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Phe Ala Asp Arg Phe Gly Arg Lys Leu Cys Leu Leu Gly Thr Val Leu	
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Val Asn Ala Val Ser Gly Val Leu Met Ala Phe Ser Pro Asn Tyr Met	
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Ser Met Leu Leu Phe Arg Leu Leu Gln Gly Leu Val Ser Lys Gly Asn	
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Trp Met Ala Gly Tyr Thr Leu Ile Thr Glu Phe Val Gly Ser Gly Ser	
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Pro Pro Ala Asp Leu Lys Met Leu Ser Leu Glu Glu Asp Val Thr Glu	
315 320 325	
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Lys Leu Ser Pro Ser Phe Ala Asp Leu Phe Arg Thr Pro Arg Leu Arg	
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aag cgc acc ttc atc ctg atg tac ctg tgg ttc acg gac tct gtg ctc	1169

Lys Arg Thr Phe Ile Leu Met Tyr Leu Trp Phe Thr Asp Ser Val Leu
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Tyr Gln Gly Leu Ile Leu His Met Gly Ala Thr Ser Gly Asn Leu Tyr
365 370 375

ctg gat ttc ctt tac tcc gct ctg gtc gaa atc ccg ggg gcc ttc ata 1265
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380 385 390

gcc ctc atc acc att gac cgc gtg ggc cgc atc tac ccc atg gcc gtg 1313
Ala Leu Ile Thr Ile Asp Arg Val Gly Arg Ile Tyr Pro Met Ala Val
395 400 405

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Ser Asn Leu Leu Ala Gly Ala Ala Cys Leu Val Met Ile Phe Ile Ser
410 415 420

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Pro Asp Leu His Trp Leu Asn Ile Ile Ile Met Cys Val Gly Arg Met
425 430 435 440

gga atc acc att gca ata caa atg atc tgc ctg gtg aat gct gag ctg 1457
Gly Ile Thr Ile Ala Ile Gln Met Ile Cys Leu Val Asn Ala Glu Leu
445 450 455

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460 465 470

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Cys Asp Ile Gly Gly Ile Ile Thr Pro Phe Ile Val Phe Arg Leu Arg
475 480 485

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Leu Ala Ala Gly Val Thr Leu Leu Leu Pro Glu Thr Lys Gly Val Ala
505 510 515 520

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Leu Pro Glu Thr Met Lys Asp Ala Glu Asn Leu Gly Arg Lys Ala Lys
525 530 535

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540 545 550

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Lys Ser Pro Gly Ser Val Val Phe Arg Asn Gly Asn Trp Pro Ile Pro
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Gly Glu Arg Ile Pro Asp Val Ala Ala Leu Ser Met Gly Phe Ser Val
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Lys Glu Asp Leu Ser Trp Pro Gly Leu Ala Val Gly Asn Leu Phe His
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Arg Pro Arg Ala Thr Val Met Val Met Val Lys Gly Val Asn Lys Leu
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gct cta ccc cca ggc agt gtc att tcg tac cct ttg gag aat gca gtt 402
Ala Leu Pro Pro Gly Ser Val Ile Ser Tyr Pro Leu Glu Asn Ala Val
                        90             95             100

cct ttt agt ctt gac agt gtt gca aat tcc att cac tcc tta ttt tct 450
Pro Phe Ser Leu Asp Ser Val Ala Asn Ser Ile His Ser Leu Phe Ser
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gag gaa act cct gtt gtt ttg cag ttg gct ccc agt gag gaa aga gtg 498
Glu Glu Thr Pro Val Val Leu Gln Leu Ala Pro Ser Glu Glu Arg Val
                        120             125             130

tat atg gta ggg aag gca aac tca gtg ttt gaa gac ctt tca gtc acc 546
Tyr Met Val Gly Lys Ala Asn Ser Val Phe Glu Asp Leu Ser Val Thr
                        135             140             145             150

ttg cgc cag ctc cgt aat cgc ctg ttt caa gaa aac tct gtt ctc agt 594
Leu Arg Gln Leu Arg Asn Arg Leu Phe Gln Glu Asn Ser Val Leu Ser
                        155             160             165

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tca ctc ccc ctc aat tct ctg agt agg aac aat gaa gtt gac ctg ctc 642
Ser Leu Pro Leu Asn Ser Leu Ser Arg Asn Asn Glu Val Asp Leu Leu 180
170

ttt ctt tct gaa ctg caa gtg cta cat gat att tca agc ttg ctg tct 690
Phe Leu Ser Glu Leu Gln Val Leu His Asp Ile Ser Ser Leu Leu Ser 195
185

cgt cat aag cat cta gcc aag gat cat tct cct gat tta tat tca ctg 738
Arg His Lys His Leu Ala Lys Asp His Ser Pro Asp Leu Tyr Ser Leu 210
200

gag ctg gca ggt ttg gat gaa att ggg aag cgt tat ggg gaa gac tct 786
Glu Leu Ala Gly Leu Asp Glu Ile Gly Lys Arg Tyr Gly Glu Asp Ser 230
215 220

gaa caa ttc aga gat gct tct aag atc ctt gtt gac gct ctg caa aag 834
Glu Gln Phe Arg Asp Ala Ser Lys Ile Leu Val Asp Ala Leu Gln Lys 245
235

ttt gca gat gac atg tac agt ctt tat ggt ggg aat gca gtg gta gag 882
Phe Ala Asp Asp Met Tyr Ser Leu Tyr Gly Gly Asn Ala Val Val Glu 260
250

tta gtc act gtc aag tca ttt gac acc tcc ctc att agg aag aca agg 930
Leu Val Thr Val Lys Ser Phe Asp Thr Ser Leu Ile Arg Lys Thr Arg 275
265

act atc ctt gag gca aaa caa gcg aag aac cca gca agt ccc tat aac 978
Thr Ile Leu Glu Ala Lys Gln Ala Lys Asn Pro Ala Ser Pro Tyr Asn 290
280

ctt gca tat aag tat aat ttt gaa tat tcc gtg gtt ttc aac atg gta 1026
Leu Ala Tyr Lys Tyr Asn Phe Glu Tyr Ser Val Val Phe Asn Met Val 310
295 300

ctt tgg ata atg atc gcc ttg gcc ttg gct gtg att atc acc tct tac 1074
Leu Trp Ile Met Ile Ala Leu Ala Leu Ala Val Ile Ile Thr Ser Tyr 325
315

aat att tgg aac atg gat cct gga tat gat agc atc att tat agg atg 1122
Asn Ile Trp Asn Met Asp Pro Gly Tyr Asp Ser Ile Ile Tyr Arg Met 340
330

aca aac cag aag att cga atg gat tgaatgttac ctgtgccaga attagaaaag 1176
Thr Asn Gln Lys Ile Arg Met Asp 350
345

ggggttggaa attggctggt ttgttaaaat atatctttta gtgtgcttta aagtagatag 1236
tatactttac atttataaaa aaaaatcaaa ttttgttctt tattttgtgt gtgcctgtga 1296
tgtttttcta gagtgaatta tagtattgac gtgaatccca ctgtggtata gattccataa 1356
tatgcttgaa tattatgata tagccattta ataacattga tttcattctg tttaatgaat 1416

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atctaagaag aaactagcct tgtggagtat atagatgctt ttcattatac acacaaaaat 1836
ccctgagggg cattttgagg catgaatata aaacattttt atttcagtaa cttttccccc 1896
tgtgtaagtt actatggttt gtggtacaac ttcattctat agaattattaa gtggaagtgg 1956
gtgaattcta ctttttatgt tggagtggac caatgtctat caagagtgc aaataaagtt 2016
aatgatgatt ccaaaaac 2033

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gaaagacaac cttcaggtcc agccctggag ctggaggagt ggagccccac tctgaagacg 120
cagcctttct ccaggttctg tctctcccat tctgattctt gacaccagat gcagg atg 178
Met
1

gtg tcc tct ccc tgc acg cag gca agc tca cgg act tgc tcc cgt atc 226
Val Ser Ser Pro Cys Thr Gln Ala Ser Ser Arg Thr Cys Ser Arg Ile
5 10 15

ctg gga ctg agc ctt ggg act gca gcc ctg ttt gct gct ggg gcc aac 274
Leu Gly Leu Ser Leu Gly Thr Ala Ala Leu Phe Ala Ala Gly Ala Asn
20 25 30

gtg gca ctc ctc ctt cct aac tgg gat gtc acc tac ctg ttg agg ggc 322
Val Ala Leu Leu Leu Pro Asn Trp Asp Val Thr Tyr Leu Leu Arg Gly
35 40 45

ctc ctt ggc agg cat gcc atg ctg gga act ggg ctc tgg gga gga ggc 370
Leu Leu Gly Arg His Ala Met Leu Gly Thr Gly Leu Trp Gly Gly Gly
50 55 60 65

ctc atg gta ctc act gca gct atc ctc atc tcc ttg atg ggc tgg aga 418
Leu Met Val Leu Thr Ala Ala Ile Leu Ile Ser Leu Met Gly Trp Arg
70 75 80

tac ggc tgc ttc agt aag agt ggg ctc tgt cga agc gtg ctt act gct 466
Tyr Gly Cys Phe Ser Lys Ser Gly Leu Cys Arg Ser Val Leu Thr Ala
85 90 95

ctg ttg tca ggt ggc ctg gct tta ctt gga gcc ctg att tgc ttt gtc 514
Leu Leu Ser Gly Gly Leu Ala Leu Leu Gly Ala Leu Ile Cys Phe Val
100 105 110

act tct gga gtt gct ctg aaa gat ggt cct ttt tgc atg ttt gat gtt 562
Thr Ser Gly Val Ala Leu Lys Asp Gly Pro Phe Cys Met Phe Asp Val
115 120 125

tca tcc ttc aat cag aca caa gct tgg aaa tat ggt tac cca ttc aaa 610
Ser Ser Phe Asn Gln Thr Gln Ala Trp Lys Tyr Gly Tyr Pro Phe Lys
130 135 140 145

gac ctg cat agt agg aat tat ctg tat gac cgt tgc ctc tgg aac tcc 658
Asp Leu His Ser Arg Asn Tyr Leu Tyr Asp Arg Ser Leu Trp Asn Ser
150 155 160

gtc tgc ctg gag ccc tct gca gct gtt gtc tgg cac gtg tcc ctc ttc 706
Val Cys Leu Glu Pro Ser Ala Ala Val Val Trp His Val Ser Leu Phe
165 170 175

tcc gcc ctt ctg tgc atc agc ctg ctc cag ctt ctc ctg gtg gtc gtt 754
Ser Ala Leu Leu Cys Ile Ser Leu Leu Gln Leu Leu Leu Val Val Val
180 185 190

cat gtc atc aac agc ctc ctg ggc ctt ttc tgc agc ctc tgc gag aag 802
His Val Ile Asn Ser Leu Leu Gly Leu Phe Cys Ser Leu Cys Glu Lys
195 200 205

tgacaggcag aaccttcact tgcaagcatg ggtgtttatc atcatcggct gtcttgaatc 862
ctttctacaa ggagtgggta cgaattataa acaaacttcc ccttttaggt 911

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Met Ala Ala Gly Leu Phe Gly Leu Ser Ala Arg Arg Leu Leu
1 5 10

gcg gca gcg gcg acg cga ggg ctc ccg gcc gcc cgc gtc cgc tgg gaa 99
Ala Ala Ala Ala Thr Arg Gly Leu Pro Ala Ala Arg Val Arg Trp Glu

15 20 25 30
tct agc ttc tcc agg act gtg gtc gcc ccg tcc gct gtg gcg gga aag 147
Ser Ser Phe Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala Gly Lys
35 40 45
cgg ccc cca gaa ccg acc aca ccg tgg caa gag gac cca gaa ccc gag 195
Arg Pro Pro Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro Glu Pro Glu
50 55 60
gac gaa aac ttg tat gag aag aac cca gac tcc cat ggt tat gac aag 243
Asp Glu Asn Leu Tyr Glu Lys Asn Pro Asp Ser His Gly Tyr Asp Lys
65 70 75
gac ccc gtt ttg gac gtc tgg aac atg cga ctt gtc ttc ttc ttt ggc 291
Asp Pro Val Leu Asp Val Trp Asn Met Arg Leu Val Phe Phe Phe Gly
80 85 90
gtc tcc atc atc ctg gtc ctt ggc agc acc ttt gtg gcc tat ctg cct 339
Val Ser Ile Ile Leu Val Leu Gly Ser Thr Phe Val Ala Tyr Leu Pro
95 100 105 110
gac tac agg tgc aca ggg tgt cca aga gcg tgg gat ggg atg aaa gag 387
Asp Tyr Arg Cys Thr Gly Cys Pro Arg Ala Trp Asp Gly Met Lys Glu
115 120 125
tgg tcc cgc cgc gaa gct gag agg ctt gtg aaa tac cga gag gcc aat 435
Trp Ser Arg Arg Glu Ala Glu Arg Leu Val Lys Tyr Arg Glu Ala Asn
130 135 140
ggc ctt ccc atc atg gaa tcc aac tgc ttc gac ccc agc aag atc cag 483
Gly Leu Pro Ile Met Glu Ser Asn Cys Phe Asp Pro Ser Lys Ile Gln
145 150 155
ctg cca gag gat gag tgaccagttg ctaagtgggg ctcaagaagc accgccttcc 538
Leu Pro Glu Asp Glu
160
ccaccccctg cctgccattc tgacctcttc tcagagcacc taattaaagg ggctgaaagt 598
601
ctg
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Met Thr Lys
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Leu Ala Gln Trp Leu Trp Gly Leu Ala Ile Leu Gly Ser Thr Trp Val
5 10 15

gcc ctg acc acg gga gcc ttg ggc ctg gag ctg ccc ttg tcc tgc cag 151
Ala Leu Thr Thr Gly Ala Leu Gly Leu Glu Leu Pro Leu Ser Cys Gln
20 25 30 35

gaa gtc ctg tgg cca ctg ccc gcc tac ttg ctg gtg tcc gcc ggc tgc 199
Glu Val Leu Trp Pro Leu Pro Ala Tyr Leu Leu Val Ser Ala Gly Cys
40 45 50

tat gcc ctg ggc act gtg ggc tat cgt gtg gcc act ttt cat gac tgc 247
Tyr Ala Leu Gly Thr Val Gly Tyr Arg Val Ala Thr Phe His Asp Cys
55 60 65

gag gac gcc gca cgc gag ctg cag agc cag ata cag gag gcc cga gcc 295
Glu Asp Ala Ala Arg Glu Leu Gln Ser Gln Ile Gln Glu Ala Arg Ala
70 75 80

gac tta gcc cgc agg ggg ctg cgc ttc tgacagccta accccattcc 342
Asp Leu Ala Arg Arg Gly Leu Arg Phe
85 90

tgtgaggaca gcccttcctc ccatttccca ttaaagagcc agtttatattt ct 394

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<212> DNA
<213> Homo sapiens

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atgccctcca aatccttggt t atg gaa tat ttg gct cat ccc agt aca ctc 111
Met Glu Tyr Leu Ala His Pro Ser Thr Leu
1 5 10

ggc ttg gct gtt gga gtt gct tgt ggc atg tgc ctg ggc tgg agc ctt 159
Gly Leu Ala Val Gly Val Ala Cys Gly Met Cys Leu Gly Trp Ser Leu
15 20 25

cga gta tgc ttt ggg atg ctc ccc aaa agc aag acg agc aag aca cac 207
Arg Val Cys Phe Gly Met Leu Pro Lys Ser Lys Thr Ser Lys Thr His
30 35 40

aca gat act gaa agt gaa gca agc atc ttg gga gac agc ggg gag tac 255
Thr Asp Thr Glu Ser Glu Ala Ser Ile Leu Gly Asp Ser Gly Glu Tyr
45 50 55

aag atg att ctt gtg gtt cga aat gac tta aag atg gga aaa ggg aaa 303
Lys Met Ile Leu Val Val Arg Asn Asp Leu Lys Met Gly Lys Gly Lys

60 65 70
gtg gct gcc cag tgc tct cat gct gct gtt tca gcc tac aag cag att 351
Val Ala Ala Gln Cys Ser His Ala Ala Val Ser Ala Tyr Lys Gln Ile 90
75 80 85
caa aga aga aat cct gaa atg ctc aaa caa tgg gaa tac tgt ggc cag 399
Gln Arg Arg Asn Pro Glu Met Leu Lys Gln Trp Glu Tyr Cys Gly Gln 105
95 100
ccc aag gtg gtg gtc aaa gct cct gat gaa gaa acc ctg att gca tta 447
Pro Lys Val Val Val Lys Ala Pro Asp Glu Glu Thr Leu Ile Ala Leu 120
110 115
ttg gcc cat gca aaa atg ctg gga ctg act gta agt tta att caa gat 495
Leu Ala His Ala Lys Met Leu Gly Leu Thr Val Ser Leu Ile Gln Asp 135
125 130
gct gga cgt act cag att gca cca ggc tct caa act gtc cta ggg att 543
Ala Gly Arg Thr Gln Ile Ala Pro Gly Ser Gln Thr Val Leu Gly Ile 150
140 145
ggg cca gga cca gca gac cta att gac aaa gtc act ggt cac cta aaa 591
Gly Pro Gly Pro Ala Asp Leu Ile Asp Lys Val Thr Gly His Leu Lys 170
155 160 165
ctt tac taggtggact ttgatatgac aacaaccct ccatcacaag tgtttgaagc 647
Leu Tyr
ctgtcagatt ctaacaacaa aagctgaatt tcttcaccca acttaaagt tcttgagatg 707
732
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<220>
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aataaagtta caactttgaa gagagtttct gcaagacatg acacaaagct gctagcagaa 120
aatcaaaacg ctgattaaaa gaagcacggt atg atg acc aaa cat aaa aag tgt 174
Met Met Thr Lys His Lys Lys Cys 5
1
ttt ata att gtt ggt gtt tta ata aca act aat att att act ctg ata 222
Phe Ile Ile Val Gly Val Leu Ile Thr Thr Asn Ile Ile Thr Leu Ile 20
10 15
gtt aaa cta act cga gat tct cag agt tta tgc ccc tat gat tgg att 270

Val Lys Leu Thr Arg Asp Ser Gln Ser Leu Cys Pro Tyr Asp Trp Ile
25 30 35 40

ggt ttc caa aac aaa tgc tat tat ttc tct aaa gaa gaa gga gat tgg 318
Gly Phe Gln Asn Lys Cys Tyr Tyr Phe Ser Lys Glu Glu Gly Asp Trp
45 50 55

aat tca agt aaa tac aac tgt tcc act caa cat gcc gac cta act ata 366
Asn Ser Ser Lys Tyr Asn Cys Ser Thr Gln His Ala Asp Leu Thr Ile
60 65 70

att gac aac ata gaa gaa atg aat ttt ctt agg cgg tat aaa tgc agt 414
Ile Asp Asn Ile Glu Glu Met Asn Phe Leu Arg Arg Tyr Lys Cys Ser
75 80 85

tct gat cac tgg att gga ctg aag atg gca aaa aat cga aca gga caa 462
Ser Asp His Trp Ile Gly Leu Lys Met Ala Lys Asn Arg Thr Gly Gln
90 95 100

tgg gta gat gga gct aca ttt acc aaa tcg ttt ggc atg aga ggg agt 510
Trp Val Asp Gly Ala Thr Phe Thr Lys Ser Phe Gly Met Arg Gly Ser
105 110 115 120

gaa gga tgt gcc tac ctc agc gat gat ggt gca gca aca gct aga tgt 558
Glu Gly Cys Ala Tyr Leu Ser Asp Asp Gly Ala Ala Thr Ala Arg Cys
125 130 135

tac acc gaa aga aaa tgg att tgc agg aaa aga ata cac taagttaatg 607
Tyr Thr Glu Arg Lys Trp Ile Cys Arg Lys Arg Ile His
140 145

tctaagataa tggggaaaat agaaaataac attattaagt gtaaaaccag caaagtactt 667
697

ttttaattaa acaaagttcg agttttgtac

<210> 62
<211> 1186
<212> DNA
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<220>
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<222> (139)..(702)

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agccggttttc gtttcaacttt tcttggtgt agagcgcttt cccctggcg ggtgagagt 120
cagagacgaa ggtgcgag atg agc act atg ttc gcg gac act ctc ctc atc 171
Met Ser Thr Met Phe Ala Asp Thr Leu Leu Ile
1 5 10

gtt ttt atc tct gtg tgc acg gct ctg ctc gca gag ggc ata acc tgg 219
Val Phe Ile Ser Val Cys Thr Ala Leu Leu Ala Glu Gly Ile Thr Trp
15 20 25

gtc ctg gtt tac agg aca gac aag tac aag aga ctg aag gca gaa gtg 267
Val Leu Val Tyr Arg Thr Asp Lys Tyr Lys Arg Leu Lys Ala Glu Val
30 35 40

gaa aaa cag agt aaa aaa ttg gaa aag aag aag gaa aca ata aca gag 315
Glu Lys Gln Ser Lys Lys Leu Glu Lys Lys Lys Glu Thr Ile Thr Glu
45 50 55

tca gct ggt cga caa cag aaa aag aaa ata gag aga caa gaa gag aaa 363
Ser Ala Gly Arg Gln Gln Lys Lys Lys Ile Glu Arg Gln Glu Glu Lys
60 65 70 75

ctg aag aat aac aac aga gat cta tca atg gtt cga atg aaa tcc atg 411
Leu Lys Asn Asn Asn Arg Asp Leu Ser Met Val Arg Met Lys Ser Met
80 85 90

ttt gct att ggc ttt tgt ttt act gcc cta atg gga atg ttc aat tcc 459
Phe Ala Ile Gly Phe Cys Phe Thr Ala Leu Met Gly Met Phe Asn Ser
95 100 105

ata ttt gat ggt aga gtg gtg gca aag ctt cct ttt acc cct ctt tct 507
Ile Phe Asp Gly Arg Val Val Ala Lys Leu Pro Phe Thr Pro Leu Ser
110 115 120

tac atc caa gga ctg tct cat cga aat ctg ctg gga gat gac acc aca 555
Tyr Ile Gln Gly Leu Ser His Arg Asn Leu Leu Gly Asp Asp Thr Thr
125 130 135

gac tgt tcc ttc att ttc ctg tat att ctc tgt act atg tcg att cga 603
Asp Cys Ser Phe Ile Phe Leu Tyr Ile Leu Cys Thr Met Ser Ile Arg
140 145 150 155

cag aac att cag aag att ctc ggc ctt gcc cct tca cga gcc gcc acc 651
Gln Asn Ile Gln Lys Ile Leu Gly Leu Ala Pro Ser Arg Ala Ala Thr
160 165 170

aag cag gca ggt gga ttt ctt ggc cca cca cct cct tct ggg aag ttc 699
Lys Gln Ala Gly Gly Phe Leu Gly Pro Pro Pro Pro Ser Gly Lys Phe
175 180 185

tct tgaactcaag aactctttat tttctatcat tctttctaga cacacacaca 752
Ser

tcagactggc aactgttttg tagcaagagc cataggtagc cttactactt gggcctcttt 812

ctagttttga attatttcta agccttttgg gtatgattag agtgaaaatg gcagccagca 872

aacttgatag tgcttttggc cctagatgat ttttatcaaa taagtggatt gattagttaa 932

gttcaggtaa tgtttatgta atgaaaaaca aatagcatcc ttcttgtttc atttacataa 992

gtattttctg tgggaccgac tctcaaggca ctgtgtatgc cctgcaagtt ggctgtctat 1052

gagcatttag agatttagaa gaaaaattta gtttgtttaa cccttgtaac tgtttgtttt 1112

gttggtgttt ttttttcaag ccaaatacat gacataagat caataaagag gccaaatttt 1172

1186

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<222> (82)..(726)

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Met Val Leu Leu Thr Met Ile Ala Arg Val 10
1 5
gcg gac ggg ctc ccg ctg gcc gcc tcg atg cag gag gac gaa cag tct 159
Ala Asp Gly Leu Pro Leu Ala Ala Ser Met Gln Glu Asp Glu Gln Ser 25
15 20
ggc cgg gac ctt caa cag tat cag agt cag gct aag caa ctc ttt cga 207
Gly Arg Asp Leu Gln Gln Tyr Gln Ser Gln Ala Lys Gln Leu Phe Arg 40
30 35
aag ttg aat gaa cag tcc cct acc aga tgt acc ttg gaa gca gga gcc 255
Lys Leu Asn Glu Gln Ser Pro Thr Arg Cys Thr Leu Glu Ala Gly Ala 55
45 50
atg act ttt cac tac att att gag cag ggg gtg tgt tat ttg gtt tta 303
Met Thr Phe His Tyr Ile Ile Glu Gln Gly Val Cys Tyr Leu Val Leu 70
60 65
tgt gaa gct gcc ttc cct aag aag ttg gct ttt gcc tac cta gaa gat 351
Cys Glu Ala Ala Phe Pro Lys Lys Leu Ala Phe Ala Tyr Leu Glu Asp 90
75 80
ttg cac tca gaa ttt gat gaa cag cat gga aag aag gtg ccc act gtg 399
Leu His Ser Glu Phe Asp Glu Gln His Gly Lys Lys Val Pro Thr Val 105
95 100
tcc cga ccc tat tcc ttt att gaa ttt gat act ttc att cag aaa acc 447
Ser Arg Pro Tyr Ser Phe Ile Glu Phe Asp Thr Phe Ile Gln Lys Thr 120
110 115
aag aag ctc tac att gac agt cgt gct cga aga aat cta ggc tcc atc 495
Lys Lys Leu Tyr Ile Asp Ser Arg Ala Arg Arg Asn Leu Gly Ser Ile 135
125 130
aac act gaa ttg caa gat gtg cag agg atc atg gtg gcc aat att gaa 543
Asn Thr Glu Leu Gln Asp Val Gln Arg Ile Met Val Ala Asn Ile Glu 150
140 145
gaa gtg tta caa cga gga gaa gca ctc tca gca ttg gat tca aag gct 591

Glu Val Leu Gln Arg Gly Glu Ala Leu Ser Ala Leu Asp Ser Lys Ala
155 160 165 170
aac aat ttg tcc agt ctg tcc aag aaa tac cgc cag gat gcg aag tac 639
Asn Asn Leu Ser Ser Leu Ser Lys Lys Tyr Arg Gln Asp Ala Lys Tyr
175 180 185
ttg aac atg cgt tcc act tat gcc aaa ctt gca gca gta gct gta ttt 687
Leu Asn Met Arg Ser Thr Tyr Ala Lys Leu Ala Ala Val Ala Val Phe
190 195 200
ttc atc atg tta ata gtg tat gtc cga ttc tgg tgg ctg tgaaataatg 736
Phe Ile Met Leu Ile Val Tyr Val Arg Phe Trp Trp Leu
205 210 215
aatacagtca ctggtaaggg agaacctaga acccagtagg tgtatatattt caggaaactg 796
agctcacaga gatgtgtatt agaatccaag tggaacttct gcctctaaag accttgcaag 856
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agatcttgtc tattggcccc ttagagaaagt taacctttgt tgttttcctt ttataatttg 1336
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<211> 974
<212> DNA
<213> Homo sapiens

<220>
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cggcgacacc tcgcagtcac tcttgcggtc tgcgcgcct ttagacagc cggggccttc 120
gtgagaccgg tgcaggcctg gggtagctc ctgtctggac agagaagaga aaa atg 176
Met
1

cag gac act ggc tca gta gtg cct ttg cat tgg ttt ggc ttt ggc tac 224
Gln Asp Thr Gly Ser Val Val Pro Leu His Trp Phe Gly Phe Gly Tyr
5 10 15

gca gca ctg gtt gct tct ggt ggg atc att ggc tat gta aaa gca ggc 272
Ala Ala Leu Val Ala Ser Gly Gly Ile Ile Gly Tyr Val Lys Ala Gly
20 25 30

agc gtg ccg tcc ctg gct gca ggg ctg ctc ttt ggc agt cta gcc ggc 320
Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu Ala Gly
35 40 45

ctg ggt gct tac cag ctg tct cag gat cca agg aac gtt tgg gtt ttc 368
Leu Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val Trp Val Phe
50 55 60 65

cta gct aca tct ggt acc ttg gct ggc att atg gga atg agg ttc tac 416
Leu Ala Thr Ser Gly Thr Leu Ala Gly Ile Met Gly Met Arg Phe Tyr
70 75 80

cac tct gga aaa ttc atg cct gca ggt tta att gca ggt gcc agt ttg 464
His Ser Gly Lys Phe Met Pro Ala Gly Leu Ile Ala Gly Ala Ser Leu
85 90 95

ctg atg gtc gcc aaa gtt gga gtt agt atg ttc aac aga ccc cat 509
Leu Met Val Ala Lys Val Gly Val Ser Met Phe Asn Arg Pro His
100 105 110

tagcagaagt catgttccag cttagactga tgaagaatta aaaatctgca tcttccacta 569
ttttcaatat attaagagaa ataagtgcag catttttgca tctgacattt tacctaaaaa 629
aaaagacacc aaacttgcca gagaggtgga aaatcagtca tgattacaaa cctacagagg 689
tggcgagtat gtaacacaag agcttaataa gaccctcata gagcttgatt cttgtatatt 749
gatgttgtct tttctttctg tatctgtagg taaatctcaa gggtaaaatg ttaggtgtca 809
gctttcaggg ctctgaaacc ctattccctg ctctgaggaa cagtgtgaaa aaaagtcttt 869
taggagattt acaatatctg ttcttttgct catcttagac cacagactga ctttgaaatt 929
atgttaagtg aaatatcaat gtaaataaag ttactataa ataata 974

<210> 65
<211> 925
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (121)..(462)

<400> 65
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ccgcgggcct tcggcagatg caggcctggg gtagtctcct ttctggactg agaagagaag 120
 atg gag aag ccc ctc ttc cca tta gtg cct ttg cat tgg ttt ggc ttt 168
 Met Glu Lys Pro Leu Phe Pro Leu Val Pro Leu His Trp Phe Gly Phe 15
 1 5 10
 ggc tac aca gca ctg gtt gtt tct ggt ggg atc gtt ggc tat gta aaa 216
 Gly Tyr Thr Ala Leu Val Val Ser Gly Gly Ile Val Gly Tyr Val Lys 30
 20 25
 aca ggc agc gtg ccg tcc ctg gca gca ggg ctg ctc ttc ggc agt cta 264
 Thr Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu 45
 35 40
 gcc ggc ctg ggt gct tac cag ctg tat cag gat cct agg aac gtt tgg 312
 Ala Gly Leu Gly Ala Tyr Gln Leu Tyr Gln Asp Pro Arg Asn Val Trp 60
 50 55
 ggt ttc cta gcc gct aca tct gtt act ttt gtt ggt gtt atg gga ata 360
 Gly Phe Leu Ala Ala Thr Ser Val Thr Phe Val Gly Val Met Gly Ile 80
 65 70 75
 aga tcc tac tac tat gga aaa ttc atg cct gta ggt tta att gca ggt 408
 Arg Ser Tyr Tyr Tyr Gly Lys Phe Met Pro Val Gly Leu Ile Ala Gly 95
 85 90
 gcc agt ttg ctg atg gcc gcc aaa gtt gga gtt cgt atg ttg atg aca 456
 Ala Ser Leu Leu Met Ala Ala Lys Val Gly Val Arg Met Leu Met Thr 110
 100
 tct gat tagcagaagt catgttcgca gcttggactc atgaaggatt aaaaatctgc 512
 Ser Asp
 atcttccact attttcaatg tattaagaga aataagtgca gcatttttgc atctgacatt 572
 ttacctaaaa aaaaaaagac accaaatttg gcggagggggt ggaaaatcag ttgttaccat 632
 tataacccta cagaggtggt gagcatgtaa catgagctta ttgagaccat catagagatc 692
 gattcttgta tattgatttt atctctttct gtatctatag gttaaattctca agggtaaaat 752
 gttaggtggt gacattgaga accctgaaac ccattccct gctcagagga acagtgtgaa 812
 aaaaaatctc ttgagagatt tagaatatct tttcttttgc tcatcttaga ccacagactg 872
 actttgaaat tatgttaagt gaaatatcaa tgaaaataaa gtttactata aat 925

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (10)..(990)

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Met Ala Ala Ala Ala Ala Ala Ala Thr Asn Gly Thr
1 5 10

gga gga agc agc ggg atg gag gtg gat gca gca gta gtc ccc agc gtg 99
Gly Gly Ser Ser Gly Met Glu Val Asp Ala Ala Val Val Pro Ser Val
15 20 25 30

atg gcc tgc gga gtg act ggg agt gtt tcc gtc gct ctc cat ccc ctt 147
Met Ala Cys Gly Val Thr Gly Ser Val Ser Val Ala Leu His Pro Leu
35 40 45

gtc att ctc aac atc tca gac cac tgg atc cgc atg cgc tcc cag gag 195
Val Ile Leu Asn Ile Ser Asp His Trp Ile Arg Met Arg Ser Gln Glu
50 55 60

ggg cgg cct gtg cag gtg att ggg gct ctg att ggc aag cag gag ggc 243
Gly Arg Pro Val Gln Val Ile Gly Ala Leu Ile Gly Lys Gln Glu Gly
65 70 75

cga aat atc gag gtg atg aac tcc ttt gag ctg ctg tcc cac acc gtg 291
Arg Asn Ile Glu Val Met Asn Ser Phe Glu Leu Leu Ser His Thr Val
80 85 90

gaa gag aag att atc att gac aag gaa tat tat tac acc aag gag gag 339
Glu Glu Lys Ile Ile Ile Asp Lys Glu Tyr Tyr Tyr Thr Lys Glu Glu
95 100 105 110

cag ttt aaa cag gtg ttc aag gag ctg gag ttt ctg ggt tgg tat acc 387
Gln Phe Lys Gln Val Phe Lys Glu Leu Glu Phe Leu Gly Trp Tyr Thr
115 120 125

aca ggg ggg cca cct gac ccc tcg gac atc cac gtc cat aag cag gtg 435
Thr Gly Gly Pro Pro Asp Pro Ser Asp Ile His Val His Lys Gln Val
130 135 140

tgt gag atc atc gag agc ccc ctc ttt ctg aag ttg aac cct atg acc 483
Cys Glu Ile Ile Glu Ser Pro Leu Phe Leu Lys Leu Asn Pro Met Thr
145 150 155

aag cac aca gat ctt cct gtc agc gtt ttt gag tct gtc att gat ata 531
Lys His Thr Asp Leu Pro Val Ser Val Phe Glu Ser Val Ile Asp Ile
160 165 170

atc aat gga gag gcc aca atg ctg ttt gct gag ctg acc tac act ctg 579
Ile Asn Gly Glu Ala Thr Met Leu Phe Ala Glu Leu Thr Tyr Thr Leu
175 180 185 190

gcc aca gag gaa gcg gaa cgc att ggt gta gac cac gta gcc cga atg 627
Ala Thr Glu Glu Ala Glu Arg Ile Gly Val Asp His Val Ala Arg Met
195 200 205

aca gca aca ggc agt gga gag aac tcc act gtg gct gaa cac ctg ata 675
Thr Ala Thr Gly Ser Gly Glu Asn Ser Thr Val Ala Glu His Leu Ile
210 215 220

gca cag cac agc gcc atc aag atg ctg cac agc cgc gtc aag ctc atc 723
Ala Gln His Ser Ala Ile Lys Met Leu His Ser Arg Val Lys Leu Ile
225 230 235

ttg gag tac gtc aag gcc tct gaa gcg gga gag gtc ccc ttt aat cat 771
Leu Glu Tyr Val Lys Ala Ser Glu Ala Gly Glu Val Pro Phe Asn His
240 245 250

gag atc ctg cgg gag gcc tat gct ctg tgt cac tgt ctc ccg gtg ctc 819
Glu Ile Leu Arg Glu Ala Tyr Ala Leu Cys His Cys Leu Pro Val Leu
255 260 265 270

agc aca gac aag ttc aag aca gat ttt tat gat caa tgc aac gac gtg 867
Ser Thr Asp Lys Phe Lys Thr Asp Phe Tyr Asp Gln Cys Asn Asp Val
275 280 285

ggg ctc atg gcc tac ctc ggc acc atc acc aaa acg tgc aac acc atg 915
Gly Leu Met Ala Tyr Leu Gly Thr Ile Thr Lys Thr Cys Asn Thr Met
290 295 300

aac cag ttt gtg aac aag ttc aat gtc ctc tac gac cga caa ggc atc 963
Asn Gln Phe Val Asn Lys Phe Asn Val Leu Tyr Asp Arg Gln Gly Ile
305 310 315

ggc agg aga atg cgc ggg ctc ttt ttc tgatgagggg acttgaaggg 1010
Gly Arg Arg Met Arg Gly Leu Phe Phe
320 325

ctgatggaca ggggtcaggc aactatccca aaggggaggg cactacactt ccttgagaga 1070
aaccactgtc attaataaaaa ggggagcagc ccctgagcac ccctg 1115

<210> 67
<211> 1721
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (6)..(1124)

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Met Thr Leu Cys Ala Met Leu Pro Leu Leu Leu Phe Thr Tyr Leu
1 5 10 15

aac tcc ttc ctg cat cag agg atc ccc cag tcc gta cgg atc ctg ggc 98
Asn Ser Phe Leu His Gln Arg Ile Pro Gln Ser Val Arg Ile Leu Gly.
20 25 30

agc ctg gtg gcc atc ctg ctg gtg ttt ctg atc act gcc atc ctg gtg 146
Ser Leu Val Ala Ile Leu Leu Val Phe Leu Ile Thr Ala Ile Leu Val
35 40 45

aag gtg cag ctg gat gct ctg ccc ttc ttt gtc atc acc atg atc aag 194

Lys Val Gln Leu Asp Ala Leu Pro Phe Phe Val Ile Thr Met Ile Lys
50 55 60

atc gtg ctc att aat tca ttt ggt gcc atc ctg cag ggc agc ctg ttt 242
Ile Val Leu Ile Asn Ser Phe Gly Ala Ile Leu Gln Gly Ser Leu Phe
65 70 75

ggg ctg gct ggc ctt ctg cct gcc agc tac acg gcc ccc atc atg agt 290
Gly Leu Ala Gly Leu Leu Pro Ala Ser Tyr Thr Ala Pro Ile Met Ser
80 85 90 95

ggc cag ggc cta gca ggc ttc ttt gcc tcc gtg gcc atg atc tgc gct 338
Gly Gln Gly Leu Ala Gly Phe Phe Ala Ser Val Ala Met Ile Cys Ala
100 105 110

att gcc agt ggc tgc gag cta tca gaa agt gcc ttc ggc tac ttt atc 386
Ile Ala Ser Gly Ser Glu Leu Ser Glu Ser Ala Phe Gly Tyr Phe Ile
115 120 125

aca gcc tgt gct gtt atc att ttg acc atc atc tgt tac ctg ggc ctg 434
Thr Ala Cys Ala Val Ile Ile Leu Thr Ile Ile Cys Tyr Leu Gly Leu
130 135 140

ccc cgc ctg gaa ttc tac cgc tac tac cag cag ctc aag ctt gaa gga 482
Pro Arg Leu Glu Phe Tyr Arg Tyr Tyr Gln Gln Leu Lys Leu Glu Gly
145 150 155

ccc ggg gag cag gag acc aag ttg gac ctc att agc aaa gga gag gag 530
Pro Gly Glu Gln Glu Thr Lys Leu Asp Leu Ile Ser Lys Gly Glu Glu
160 165 170 175

cca aga gca ggc aaa gag gaa tct gga gtt tca gtc tcc aac tct cag 578
Pro Arg Ala Gly Lys Glu Glu Ser Gly Val Ser Val Ser Asn Ser Gln
180 185 190

ccc acc aat gaa agc cac tct atc aaa gcc atc ctg aaa aat atc tca 626
Pro Thr Asn Glu Ser His Ser Ile Lys Ala Ile Leu Lys Asn Ile Ser
195 200 205

gtc ctg gct ttc tct gtc tgc ttc atc ttc act atc acc att ggg atg 674
Val Leu Ala Phe Ser Val Cys Phe Ile Phe Thr Ile Thr Ile Gly Met
210 215 220

ttt cca gcc gtg act gtt gag gtc aag tcc agc atc gca ggc agc agc 722
Phe Pro Ala Val Thr Val Glu Val Lys Ser Ser Ile Ala Gly Ser Ser
225 230 235

acc tgg gaa cgt tac ttc att cct gtg tcc tgt ttc ttg act ttc aat 770
Thr Trp Glu Arg Tyr Phe Ile Pro Val Ser Cys Phe Leu Thr Phe Asn
240 245 250 255

atc ttt gac tgg ttg ggc cgg agc ctc aca gct gta ttc atg tgg cct 818
Ile Phe Asp Trp Leu Gly Arg Ser Leu Thr Ala Val Phe Met Trp Pro
260 265 270

ggg aag gac agc cgc tgg ctg cca agc ctg gtg ctg gcc cgg ctg gtg 866
Gly Lys Asp Ser Arg Trp Leu Pro Ser Leu Val Leu Ala Arg Leu Val

275 280 285
ttt gtg cca ctg ctg ctg ctg tgc aac att aag ccc cgc cgc tac ctg 914
Phe Val Pro Leu Leu Leu Leu Cys Asn Ile Lys Pro Arg Arg Tyr Leu
290 295 300
act gtg gtc ttc gag cac gat gcc tgg ttc atc ttc ttc atg gct gcc 962
Thr Val Val Phe Glu His Asp Ala Trp Phe Ile Phe Phe Met Ala Ala
305 310 315
ttt gcc ttc tcc aac ggc tac ctc gcc agc ctc tgc atg tgc ttc ggg 1010
Phe Ala Phe Ser Asn Gly Tyr Leu Ala Ser Leu Cys Met Cys Phe Gly
320 325 330 335
ccc aag aaa gtg aag cca gct gag gca gag acc gca gga gcc atc atg 1058
Pro Lys Lys Val Lys Pro Ala Glu Ala Glu Thr Ala Gly Ala Ile Met
340 345 350
gcc ttc ttc ctg tgt ctg ggt ctg gca ctg ggg gct gtt ttc tcc ttc 1106
Ala Phe Phe Leu Cys Leu Gly Leu Ala Leu Gly Ala Val Phe Ser Phe
355 360 365
ctg ttc cgg gca att gtg tgacaaagga tggacagaag gactgcctgc 1154
Leu Phe Arg Ala Ile Val
370
ctccctccct gtctgcctcc tgcccttcc ttctgccagg ggtgatcctg agtggctctgg 1214
cggttttttc ttctaactga cttctgcttt ccacggcgtg tgctgggccc ggcctccag 1274
gccctgggga gggagcctct ggacggacag tggggacatt gtgggtttgg ggctcagagt 1334
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tccctgcttg tgcaggccag tggaggctct tgggcttgga gaacacgtgt gtctctgtgt 1454
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gagctgggtc tgaccgttgt atggtttgac ctgatatact ccattctccc ctgcgcctcc 1574
tctctgtgt tctctccatg tccccctccc aactcccat gccagttct taccatcat 1634
gcaccctgta cagttgccac gttactgcct tttttaaaaa tatatttgac agaaaccagg 1694
tgccctcaga ggctctctga tttaaat 1721

<210> 68
<211> 1504
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (63)..(611)

<400> 68

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gc atg aag ctc tta tct ttg gtg gct gtg gtc ggg tgt ttg ctg gtg 107
Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val 15
1 5 10
ccc cca gct gaa gcc aac aag agt tct gaa gat atc cgg tgc aaa tgc 155
Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys 30
20 25
atc tgt cca cct tat aga aac atc agt ggg cac att tac aac cag aat 203
Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn 45
35 40
gta tcc cag aag gac tgc aac tgc ctg cac gtg gtg gag ccc atg cca 251
Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro 60
50 55
gtg cct ggc cat gac gtg gag gcc tac tgc ctg ctg tgc gag tgc agg 299
Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg 75
65 70
tac gag gag cgc agc acc acc acc atc aag gtc atc att gtc atc tac 347
Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr 95
80 85 90
ctg tcc gtg gtg ggt gcc ctg ttg ctc tac atg gcc ttc ctg atg ctg 395
Leu Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu 110
100 105
gtg gac cct ctg atc cga aag ccg gat gca tac act gag caa ctg cac 443
Val Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His 125
115
aat gag gag gag aat gag gat gct cgc tct atg gca gca gct gct gca 491
Asn Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala 140
130 135
tcc ctc ggg gga ccc cga gca aac aca gtc ctg gag cgt gtg gaa ggt 539
Ser Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly 155
145 150
gcc cag cag cgg tgg aag ctgcag gtg cag gag cag cgg aag aca gtc 587
Ala Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val 175
160 165 170
ttc gat cgg cac aag atg ctc agc tagatgggct ggtgtggttg ggtcaaggcc 641
Phe Asp Arg His Lys Met Leu Ser 180
ccaacaccat ggctgccagc ttccaggctg gacaaagcag ggggctactt ctcccttccc 701
tcggttccag tcttcccttt aaaagcctgt ggcatTTTTc ctcccttctcc ctaactttag 761
aaatgttgta cttggctatt ttgattaggg aagagggatg tggctctctga tctctgttgt 821
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tgtccacagt cactgagcca gacggtcggg ttgaacatga gactcgaggc tgagcgtgga 1361
tctgaacacc acagcccctg tacttgggtt gcctcttgct cctgaacttc gttgtaccag 1421
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cattaaattg ttttatttct ctc 1504

<210> 69
<211> 532
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (93)..(440)

<400> 69
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cccgttgaa gcaagggagc ccagccggag cc atg gcc agt aca gtg gta gca 113
Met Ala Ser Thr Val Val Ala
1 5

gtt gga ctg acc att gct gct gca gga ttt gca ggc cgt tac gtt ttg 161
Val Gly Leu Thr Ile Ala Ala Ala Gly Phe Ala Gly Arg Tyr Val Leu
10 15 20

caa gcc atg aag cat atg gag cct caa gta aaa caa gtt ttt caa agc 209
Gln Ala Met Lys His Met Glu Pro Gln Val Lys Gln Val Phe Gln Ser
25 30 35

cta cca aaa tct gcc ttc agt ggt ggc tat tat aga ggt ggg ttt gaa 257
Leu Pro Lys Ser Ala Phe Ser Gly Gly Tyr Tyr Arg Gly Gly Phe Glu
40 45 50 55

ccc aaa atg aca aaa cgg gaa gca gca tta ata cta ggt gta agc cct 305
Pro Lys Met Thr Lys Arg Glu Ala Ala Leu Ile Leu Gly Val Ser Pro
60 65 70

act gcc aat aaa ggg aaa ata aga gat gct cat cga cga att atg ctt 353

Thr Ala Asn Lys Gly Lys Ile Arg Asp Ala His Arg Arg Ile Met Leu
75 80 85
tta aat cat cct gac aaa gga gga tct cct tat ata gca gcc aaa atc 401
Leu Asn His Pro Asp Lys Gly Gly Ser Pro Tyr Ile Ala Ala Lys Ile
90 95 100
aat gaa gct aaa gat tta cta gaa ggt caa gct aaa aaa tgaagtaaat 450
Asn Glu Ala Lys Asp Leu Leu Glu Gly Gln Ala Lys Lys
105 110 115
gtatgatgaa ttttaagttc gtattagttt atgtatatga gtactaagtt tttataataa 510
532
aatgcctcag agctacaatt tt

<210> 70
<211> 662
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (92)..(547)

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tccagctggt cgaaggtgat ccagacgcaa g atg gct gtc ctc tct aag gaa 112
Met Ala Val Leu Ser Lys Glu
1 5

tat ggt ttt gtg ctt cta act ggt gct gcc agc ttt ata atg gtg gcc 160
Tyr Gly Phe Val Leu Leu Thr Gly Ala Ala Ser Phe Ile Met Val Ala
10 15 20

cac cta gcc atc aat gtt tcc aag gcc cgc aag aag tac aaa gtg gag 208
His Leu Ala Ile Asn Val Ser Lys Ala Arg Lys Lys Tyr Lys Val Glu
25 30 35

tat cct atc atg tac agc acg gac cct gaa aat ggg cac atc ttc aac 256
Tyr Pro Ile Met Tyr Ser Thr Asp Pro Glu Asn Gly His Ile Phe Asn
40 45 50 55

tgc att cag cga gcc cac cag aac acg ttg gaa gtg tat cct ccc ttc 304
Cys Ile Gln Arg Ala His Gln Asn Thr Leu Glu Val Tyr Pro Pro Phe
60 65 70

tta ttt ttt cta gct gtt gga ggt gtt tac cac ccg cgt ata gct tct 352
Leu Phe Phe Leu Ala Val Gly Gly Val Tyr His Pro Arg Ile Ala Ser
75 80 85

ggc ctg ggc ttg gcc tgg att gtt gga cga gtt ctt tat gct tat ggc 400
Gly Leu Gly Leu Ala Trp Ile Val Gly Arg Val Leu Tyr Ala Tyr Gly
90 95 100

tat tac acg gga gaa ccc agc aag cgt agt cga gga gcc ctg ggg tcc 448

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Tyr Tyr Thr Gly Glu Pro Ser Lys Arg Ser Arg Gly Ala Leu Gly Ser
105 110 115
atc gcc ctc ctg ggc ttg gtg ggc aca act gtg tgc tct gct ttc cag 496
Ile Ala Leu Leu Gly Leu Val Gly Thr Thr Val Cys Ser Ala Phe Gln
120 125 130 135
cat ctt ggt tgg gtt aaa agt ggc ttg ggc agt gga ccc aaa tgc tgc 544
His Leu Gly Trp Val Lys Ser Gly Leu Gly Ser Gly Pro Lys Cys Cys
140 145 150
cat taaagaatta taggggttta aaaactctca ttcatttta atgacttacc 597
His
tttatttcca gttacatttt ttttctaaat ataataaaaa cttacctggc atcagcctca 657
662
tacct

<210> 71
<211> 2373
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (134)..(1810)

<400> 71
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gctcggggcc agc atg gcc ccc acg ctg caa cag gcg tac cgg agg cgc 169
Met Ala Pro Thr Leu Gln Gln Ala Tyr Arg Arg Arg
1 5 10
tgg tgg atg gcc tgc acg gct gtg ctg gag aac ctc ttc ttc tct gct 217
Trp Trp Met Ala Cys Thr Ala Val Leu Glu Asn Leu Phe Phe Ser Ala
15 20 25
gta ctc ctg ggc tgg ggc tcc ctg ttg atc att ctg aag aac gag ggc 265
Val Leu Leu Gly Trp Gly Ser Leu Leu Ile Ile Leu Lys Asn Glu Gly
30 35 40
ttc tat tcc agc acg tgc cca gct gag agc agc acc aac acc acc cag 313
Phe Tyr Ser Ser Thr Cys Pro Ala Glu Ser Ser Thr Asn Thr Thr Gln
45 50 55 60
gat gag cag cgc agg tgg cca ggc tgt gac cag cag gac gag atg ctc 361
Asp Glu Gln Arg Trp Pro Gly Cys Asp Gln Gln Asp Glu Met Leu
65 70 75
aac ctg ggc ttc acc att ggt tcc ttc gtg ctc agc gcc acc acc ctg 409
Asn Leu Gly Phe Thr Ile Gly Ser Phe Val Leu Ser Ala Thr Thr Leu
80 85 90

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cca ctg ggg atc ctc atg gac cgc ttt ggc ccc cga ccc gtg cgg ctg Pro Leu Gly Ile Leu Met Asp Arg Phe Gly Pro Arg Pro Val Arg Leu 95 100 105	457
gtt ggc agt gcc tgc ttc act gcg tcc tgc acc ctc atg gcc ctg gcc Val Gly Ser Ala Cys Phe Thr Ala Ser Cys Thr Leu Met Ala Leu Ala 110 115 120	505
tcc cgg gac gtg gaa gct ctg tct ccg ttg ata ttc ctg gcg ctg tcc Ser Arg Asp Val Glu Ala Leu Ser Pro Leu Ile Phe Leu Ala Leu Ser 125 130 135 140	553
ctg aat ggc ttt ggt ggc atc tgc cta acg ttc act tca ctc acg ctg Leu Asn Gly Phe Gly Gly Ile Cys Leu Thr Phe Thr Ser Leu Thr Leu 145 150 155	601
ccc aac atg ttt ggg aac ctg cgc tcc acg tta atg gcc ctc atg att Pro Asn Met Phe Gly Asn Leu Arg Ser Thr Leu Met Ala Leu Met Ile 160 165 170	649
ggc tct tac gcc tct tct gcc att acg ttc cca gga atc aag ctg atc Gly Ser Tyr Ala Ser Ser Ala Ile Thr Phe Pro Gly Ile Lys Leu Ile 175 180 185	697
tac gat gcc ggt gtg gcc ttc gtg gtc atc atg ttc acc tgg tct ggc Tyr Asp Ala Gly Val Ala Phe Val Val Ile Met Phe Thr Trp Ser Gly 190 195 200	745
ctg gcc tgc ctt atc ttt ctg aac tgc acc ctc aac tgg ccc atc gaa Leu Ala Cys Leu Ile Phe Leu Asn Cys Thr Leu Asn Trp Pro Ile Glu 205 210 215 220	793
gcc ttt cct gcc cct gag gaa gtc aat tac acg aag aag atc aag ctg Ala Phe Pro Ala Pro Glu Glu Val Asn Tyr Thr Lys Lys Ile Lys Leu 225 230 235	841
agt ggg ctg gcc ctg gac cac aag gtg aca ggt gac ctc ttc tac acc Ser Gly Leu Ala Leu Asp His Lys Val Thr Gly Asp Leu Phe Tyr Thr 240 245 250	889
cat gtg acc acc atg ggc cag agg ctc agc cag aag gcc ccc agc ctg His Val Thr Thr Met Gly Gln Arg Leu Ser Gln Lys Ala Pro Ser Leu 255 260 265	937
gag gac ggt tgc gat gcc ttc atg tca ccc cag gat gtt cgg gcc acc Glu Asp Gly Ser Asp Ala Phe Met Ser Pro Gln Asp Val Arg Gly Thr 270 275 280	985
tca gaa aac ctt cct gag agg tct gtc ccc tta cgc aag agc ctc tgc Ser Glu Asn Leu Pro Glu Arg Ser Val Pro Leu Arg Lys Ser Leu Cys 285 290 295 300	1033
tcc ccc act ttc ctg tgg agc ctc ctc acc atg ggc atg acc cag ctg Ser Pro Thr Phe Leu Trp Ser Leu Leu Thr Met Gly Met Thr Gln Leu 305 310 315	1081
cgg atc atc ttc tac atg gct gct gtg aac aag atg ctg gag tac ctt	1129

Arg Ile Ile Phe Tyr Met Ala Ala Val Asn Lys Met Leu Glu Tyr Leu
320 325 330

gtg act ggt ggc cag gag cat gag aca aat gaa cag caa caa aag gtg 1177
Val Thr Gly Gly Gln Glu His Glu Thr Asn Glu Gln Gln Lys Val
335 340 345

gca gag aca gtt ggg ttc tac tcc tcc gtc ttc ggg gcc atg cag ctg 1225
Ala Glu Thr Val Gly Phe Tyr Ser Ser Val Phe Gly Ala Met Gln Leu
350 355 360

ttg tgc ctt ctc acc tgc ccc ctc att ggc tac atc atg gac tgg cgg 1273
Leu Cys Leu Leu Thr Cys Pro Leu Ile Gly Tyr Ile Met Asp Trp Arg
365 370 375 380

atc aag gac tgc gtg gac gcc cca act cag ggc act gtc ctc gga gat 1321
Ile Lys Asp Cys Val Asp Ala Pro Thr Gln Gly Thr Val Leu Gly Asp
385 390 395

gcc agg gac ggg gtt gct acc aaa tcc atc aga cca cgc tac tgc aag 1369
Ala Arg Asp Gly Val Ala Thr Lys Ser Ile Arg Pro Arg Tyr Cys Lys
400 405 410

atc caa aag ctc acc aat gcc atc agt gcc ttc acc ctg acc aac ctg 1417
Ile Gln Lys Leu Thr Asn Ala Ile Ser Ala Phe Thr Leu Thr Asn Leu
415 420 425

ctg ctt gtg ggt ttt ggc atc acc tgt ctc atc aac aac tta cac ctc 1465
Leu Leu Val Gly Phe Gly Ile Thr Cys Leu Ile Asn Asn Leu His Leu
430 435 440

cag ttt gtg acc ttt gtc ctg cac acc att gtt cga ggt ttc ttc cac 1513
Gln Phe Val Thr Phe Val Leu His Thr Ile Val Arg Gly Phe Phe His
445 450 455 460

tca gcc tgt ggg agt ctc tat gct gca gtg ttc cca tcc aac cac ttt 1561
Ser Ala Cys Gly Ser Leu Tyr Ala Ala Val Phe Pro Ser Asn His Phe
465 470 475

ggg acg ctg aca ggc ctg cag tcc ctc atc agt gct gtg ttc gcc ttg 1609
Gly Thr Leu Thr Gly Leu Gln Ser Leu Ile Ser Ala Val Phe Ala Leu
480 485 490

ctt cag cag cca ctt ttc atg ggc atg gtg gga ccc ctg aaa gga gag 1657
Leu Gln Gln Pro Leu Phe Met Ala Met Val Gly Pro Leu Lys Gly Glu
495 500 505

ccc ttc tgg gtg aat ctg ggc ctc ctg cta ttc tca ctc ctg gga ttc 1705
Pro Phe Trp Val Asn Leu Gly Leu Leu Leu Phe Ser Leu Leu Gly Phe
510 515 520

ctg ttg cct tcc tac ctc ttc tat tac cgt gcc cgg ctc cag cag gag 1753
Leu Leu Pro Ser Tyr Leu Phe Tyr Tyr Arg Ala Arg Leu Gln Gln Glu
525 530 535 540

tac gcc gcc aat ggg atg ggc cca ctg aag gtg ctt agc ggc tct gag 1801
Tyr Ala Ala Asn Gly Met Gly Pro Leu Lys Val Leu Ser Gly Ser Glu

545

550

555

gtg acc gca tagacttctc agaccaaggg acctggatga caggcaatca
Val Thr Ala

1850

aggcctgagc aaccaaaagg agtgcccat atggcttttc tacctgtaac atgcacatag 1910
agccatggcc gtagatttat aaataccaag agaagttcta tttttgtaaa gactgcaaaa 1970
aggaggaaaa aaaaaccttc aaaaacgccc cctaagtcaa cgctccattg actgaagaca 2030
gtccctatcc tagaggggtt gaggcttctt cctccttggg ttggaggaga ccagggtgcc 2090
tcttatctcc ttctagcggg ctgcctcctg gtacctcttg gggggatcgg caaacaggct 2150
accctgagg tcccatgtgc catgagtgtg cacacatgca tgtgtctgtg tatgtgtgaa 2210
tgtgagagag acacagccct cctttcagaa ggaaaggggc ctgaggtgcc agctgtgtcc 2270
tgggttaggg gttgggggtc ggccccttcc agggccagga gggcagggtc cctctctggt 2330
gctgctgctt gcaagtctta gaggaataa aaagggaagt gag 2373

<210> 72
<211> 1316
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (11)..(1000)

<400> 72
gttgtccaag atg gag ggc gct cca ccg ggg tcg ctc gcc ctc cgg ctc 49
Met Glu Gly Ala Pro Pro Gly Ser Leu Ala Leu Arg Leu
1 5 10

ctg ctg ttc gtg gcg cta ccc gcc tcc ggc tgg ctg acg acg ggc gcc 97
Leu Leu Phe Val Ala Leu Pro Ala Ser Gly Trp Leu Thr Thr Gly Ala
15 20 25

ccc gag ccg ccg ccg ctg tcc gga gcc cca cag gac ggc atc aga att 145
Pro Glu Pro Pro Pro Leu Ser Gly Ala Pro Gln Asp Gly Ile Arg Ile
30 35 40 45

aat gta act aca ctg aaa gat gat ggg gac ata tct aaa cag cag gtt 193
Asn Val Thr Thr Leu Lys Asp Asp Gly Asp Ile Ser Lys Gln Gln Val
50 55 60

gtt ctt aac ata acc tat gag agt gga cag gtg tat gta aat gac tta 241
Val Leu Asn Ile Thr Tyr Glu Ser Gly Gln Val Tyr Val Asn Asp Leu
65 70 75

cct gta aat agt ggt gta acc cga ata agc tgt cag act ttg ata gtg 289
Pro Val Asn Ser Gly Val Thr Arg Ile Ser Cys Gln Thr Leu Ile Val
80 85 90

aag aat gaa aat ctt gaa aat ttg gag gaa aaa gaa tat ttt gga att 337
Lys Asn Glu Asn Leu Glu Asn Leu Glu Glu Lys Glu Tyr Phe Gly Ile
95 100 105

gtc agt gta agg att tta gtt cat gag tgg cct atg aca tct ggt tcc 385
Val Ser Val Arg Ile Leu Val His Glu Trp Pro Met Thr Ser Gly Ser
110 115 120 125

agt ttg caa cta att gtc att caa gaa gag gta gta gag att gat gga 433
Ser Leu Gln Leu Ile Val Ile Gln Glu Glu Val Val Glu Ile Asp Gly
130 135 140

aaa caa gtt cag caa aag gat gtc act gaa att gat att tta gtt aag 481
Lys Gln Val Gln Gln Lys Asp Val Thr Glu Ile Asp Ile Leu Val Lys
145 150 155

aac cgg gga gta ctc aga cat tca aac tat acc ctc cct ttg gaa gaa 529
Asn Arg Gly Val Leu Arg His Ser Asn Tyr Thr Leu Pro Leu Glu Glu
160 165 170

agc atg ctc tac tct att tct cga gac agt gac att tta ttt acc ctt 577
Ser Met Leu Tyr Ser Ile Ser Arg Asp Ser Asp Ile Leu Phe Thr Leu
175 180 185

cct aac ctc tcc aaa aaa gaa agt gtt agt tca ctg caa acc act agc 625
Pro Asn Leu Ser Lys Lys Glu Ser Val Ser Ser Leu Gln Thr Thr Ser
190 195 200 205

cag tat ctt atc agg aat gtg gaa acc act gta gat gaa gat gtt tta 673
Gln Tyr Leu Ile Arg Asn Val Glu Thr Thr Val Asp Glu Asp Val Leu
210 215 220

cct ggc aag tta cct gaa act cct ctc aga gca gag ccg cca tct tca 721
Pro Gly Lys Leu Pro Glu Thr Pro Leu Arg Ala Glu Pro Pro Ser Ser
225 230 235

tat aag gta atg tgt cag tgg atg gaa aag ttt aga aaa gat ctg tgt 769
Tyr Lys Val Met Cys Gln Trp Met Glu Lys Phe Arg Lys Asp Leu Cys
240 245 250

agg ttc tgg agc aac gtt ttc cca gta ttc ttt cag ttt ttg aac atc 817
Arg Phe Trp Ser Asn Val Phe Pro Val Phe Phe Gln Phe Leu Asn Ile
255 260 265

atg gtg gtt gga att aca gga gca gct gtg gta ata acc atc tta aag 865
Met Val Val Gly Ile Thr Gly Ala Ala Val Val Ile Thr Ile Leu Lys
270 275 280 285

gtg ttt ttc cca gtt tct gaa tac aaa gga att ctt cag ttg gat aaa 913
Val Phe Phe Pro Val Ser Glu Tyr Lys Gly Ile Leu Gln Leu Asp Lys
290 295 300

gtg gac gtc ata cct gtg aca gct atc aac tta tat cca gat ggt cca 961
Val Asp Val Ile Pro Val Thr Ala Ile Asn Leu Tyr Pro Asp Gly Pro
305 310 315

gag aaa aga gct gaa aac ctt gaa gat aaa aca tgt att taaaacgcca 1010
Glu Lys Arg Ala Glu Asn Leu Glu Asp Lys Thr Cys Ile
320 325 330
tctcatatca tggactccga agtagcctgt tgccctccaaa tttgccactt gaataataatt 1070
ttcttttaaat cgtaagaat cagtttatac actagagaaa ttgctaaact ctaagactgc 1130
ctgaaaattg acctttacag tgccaagtta aagtttacct tattctcggc cgggtgcagt 1190
ggctcatgcc tgtaatccca ggactttggg aggccaatgc gggcggatca cgaggtcaga 1250
tcaagaccat cctgccaaca tggtgaaacc ctgtctctac taaaaaaaaat aaaaaagtta 1310
1316
gctggg

<210> 73
<211> 893
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (110)..(433)

<400> 73
atcgcgagtg cgggtgcttta gtacgcgct ggcaccttta ctctcgccgg ccgcggaac 60
ccgtttgagc tcggtatcct agtgcacacg ccttgcaagc gacggcgcc atg agt ctg 118
Met Ser Leu
1

act tcc agt tcc agc gta cga gtt gaa tgg atc gca gca gtt acc att 166
Thr Ser Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala Val Thr Ile
5 10 15

gct gct ggg aca gct gca att ggt tat cta gct tac aaa aga ttt tat 214
Ala Ala Gly Thr Ala Ala Ile Gly Tyr Leu Ala Tyr Lys Arg Phe Tyr
20 25 30 35

gtt aaa gat cat cga aat aaa gct atg ata aac ctt cac atc cag aaa 262
Val Lys Asp His Arg Asn Lys Ala Met Ile Asn Leu His Ile Gln Lys
40 45 50

gac aac ccc aag ata gta cat gct ttt gac atg gag gat ttg gga gat 310
Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp Leu Gly Asp
55 60 65

aaa gct gtg tac tgc cgt tgt tgg agg tcc aaa aag ttc cca ttc tgt 358
Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe Pro Phe Cys
70 75 80

gat ggg gct cac aca aaa cat aac gaa gag act gga gac aat gtg ggc 406
Asp Gly Ala His Thr Lys His Asn Glu Glu Thr Gly Asp Asn Val Gly
85 90 95

cct ctg atc atc aag aaa aaa gaa act taaatggaca cttttgatgc 453
Pro Leu Ile Ile Lys Lys Lys Glu Thr
100 105
tgcaaatcag cttgtcgtga agttacctga ttgtttaatt agaatagacta ccacctctgt 513
ctgattcacc ttcgctggat tctaaatgtg gtatattgca aactgcagct ttcacattta 573
tggcatttgt cttgttgaaa catcgtgggt cacatttggt taaacaaaaa aaaaaaaaaa 633
aaggaaaaac caacctcatg gcctgtgggt tattttgggtc ttgtaaggat ccatttcttt 693
aaaatactga catatagagt tgtaccttat atagaatata gttgtatctt gaagtcaaca 753
tattaaatta ttctcaaaat tatgtatttg cagattgtac ttgtaagttt caaagaaaaa 813
ttaccatctt ttcattatga cctggaaact aaataggatg tgattcagct acattaattt 873
cttaatacaa tctaggaaag 893

<210> 74
<211> 690
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (230)..(532)

<400> 74
taacagcgca tgcgtgcagt gttgcctcgc ccaaagaaga ctacaatctc cagggaaacc 60
tggggcgctc cgcgcaaacg tccataactg aaagtagcta aggcacccca gccggaggaa 120
gtgagctctc ctggggcggtg gttgttcgtg atccttgcat ctgttactta gggtaagggc 180
ttgggtcttg ccccgagac ccttgggacg acccgcccc agcgagct atg aac ctg 238
Met Asn Leu
1

gag cga gtg tcc aat gag gag aaa ttg aac ctg tgc cgg aag tac tac 286
Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg Lys Tyr Tyr
5 10 15

ctg ggg ggg ttt gct ttc ctg cct ttt ctc tgg ttg gtc aac atc ttc 334
Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp Leu Val Asn Ile Phe
20 25 30 35

tgg ttc ttc cga gag gcc ttc ctt gtc cca gcc tac aca gaa cag agc 382
Trp Phe Phe Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr Glu Gln Ser
40 45 50

caa atc aaa ggc tat gtc tgg cgc tca gct gtg ggc ttc ctc ttc tgg 430
Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe Leu Phe Trp
55 60 65

gtg ata gtg ctc acc tcc tgg atc acc atc ttc cag atc tac cgg ccc 478
Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile Tyr Arg Pro
70 75 80

cgc tgg ggt gcc ctt ggg gac tac ctc tcc ttc acc ata ccc ctg ggc 526
Arg Trp Gly Ala Leu Gly Asp Tyr Leu Ser Phe Thr Ile Pro Leu Gly
85 90 95

acc ccc tgacaacttc tgcacatact ggggacctgc ttattctccc aggacaggct 582
Thr Pro
100

ccttaaagca gaggagcctg tcttgggagc cccttctcaa actcctaaga cttgttttca 642
tgtccacgt tctctgctga catcccccaa taaaggaccc taactttc 690

<210> 75
<211> 2186
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (118)..(1233)

<400> 75
actctttctt cggctcgcga gctgagagga gcaggtagag gggcagaggc gggactgtcg 60
tctgggggag cgcgccagga ggctcctcag gccgacccca gacctgggt gccagg 117

atg aag tat ctc cgg cac cgg cgg ccc aat gcc acc ctc att ctg gcc 165
Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala
1 5 10 15

atc ggc gct ttc acc ctc ctc ctc ttc agt ctg cta gtg tca cca ccc 213
Ile Gly Ala Phe Thr Leu Leu Leu Phe Ser Leu Leu Val Ser Pro Pro
20 25 30

acc tgc aag gtc cag gag cag cca ccg gcg atc ccc gag gcc ctg gcc 261
Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala
35 40 45

tgg ccc act cca ccc acc cgc cca gcc ccg gcc ccg tgc cat gcc aac 309
Trp Pro Thr Pro Pro Thr Arg Pro Ala Pro Ala Pro Cys His Ala Asn
50 55 60

acc tct atg gtc acc cac ccg gac ttc gcc acg cag ccg cag cac gtt 357
Thr Ser Met Val Thr His Pro Asp Phe Ala Thr Gln Pro Gln His Val
65 70 75 80

cag aac ttc ctc ctg tac aga cac tgc cgc cac ttt ccc ctg ctg cag 405
Gln Asn Phe Leu Leu Tyr Arg His Cys Arg His Phe Pro Leu Leu Gln
85 90 95

gac gtg ccc ccc tct aag tgc gcg cag ccg gtc ttc ctg ctg ctg gtg 453
Asp Val Pro Pro Ser Lys Cys Ala Gln Pro Val Phe Leu Leu Leu Val

100	105	110	
atc aag tcc tcc cct agc aac	tat gtg cgc cgc gag	ctg ctg cgg cgc	501
Ile Lys Ser Ser Pro Ser Asn	Tyr Val Arg Arg Glu	Leu Leu Arg Arg	
115	120	125	
acg tgg ggc cgc gag cgc aag	gta cgg ggt ttg cag	ctg cgc ctc ctc	549
Thr Trp Gly Arg Glu Arg Lys	Val Arg Gly Leu Gln	Leu Arg Leu Leu	
130	135	140	
ttc ctg gtg ggc aca gcc tcc	aac ccg cac gag gcc	cgc aag gtc aac	597
Phe Leu Val Gly Thr Ala Ser	Asn Pro His Glu Ala	Arg Lys Val Asn	
145	150	155	160
cgg ctg ctg gag ctg gag gca	cag act cac gga gac	atc ctg cag tgg	645
Arg Leu Leu Glu Leu Glu Ala	Gln Thr His Gly Asp	Ile Leu Gln Trp	
165	170	175	
gac ttc cac gac tcc ttc ttc	aac ctc acg ctc aag	cag gtc ctg ttc	693
Asp Phe His Asp Ser Phe Phe	Asn Leu Thr Leu Lys	Gln Val Leu Phe	
180	185	190	
tta cag tgg cag gag aca agg	tgc gcc aac gcc agc	ttc gtg ctc aac	741
Leu Gln Trp Gln Glu Thr Arg	Cys Ala Asn Ala Ser	Phe Val Leu Asn	
195	200	205	
ggg gat gat gac gtc ttt gca	cac aca gac aac atg	gtc ttc tac ctg	789
Gly Asp Asp Asp Val Phe Ala	His Thr Asp Asn Met	Val Phe Tyr Leu	
210	215	220	
cag gac cat gac cct ggc cgc	cac ctc ttc gtg ggg	caa ctg atc caa	837
Gln Asp His Asp Pro Gly Arg	His Leu Phe Val Gly	Gln Leu Ile Gln	
225	230	235	240
aac gtg ggc ccc atc cgg gct	ttt tgg agc aag tac	tat gtg cca gag	885
Asn Val Gly Pro Ile Arg Ala	Phe Trp Ser Lys Tyr	Tyr Val Pro Glu	
245	250	255	
gtg gtg act cag aat gag cgg	tac cca ccc tat tgt	ggg ggt ggt ggc	933
Val Val Thr Gln Asn Glu Arg	Tyr Pro Pro Tyr Cys	Gly Gly Gly Gly	
260	265	270	
ttc ttg ctg tcc cgc ttc acg	gcc gct gcc ctg cgc	cgt gct gcc cat	981
Phe Leu Leu Ser Arg Phe Thr	Ala Ala Ala Leu Arg	Arg Ala Ala His	
275	280	285	
gtc ttg gac atc ttc ccc att	gat gat gtc ttc ctg	ggt atg tgt ctg	1029
Val Leu Asp Ile Phe Pro Ile	Asp Asp Val Phe Leu	Gly Met Cys Leu	
290	295	300	
gag ctt gag gga ctg aag cct	gcc tcc cac agc ggc	atc cgc acg tct	1077
Glu Leu Glu Gly Leu Lys Pro	Ala Ser His Ser Gly	Ile Arg Thr Ser	
305	310	315	320
ggc gtg cgg gct cca tgc	caa cac ctg tcc tcc	ttt gac ccc tgc ttc	1125
Gly Val Arg Ala Pro Ser	Gln His Leu Ser Ser	Phe Asp Pro Cys Phe	
325	330	335	

tac cga gac ctg ctg ctg gtg cac cgc ttc cta cct tat gag atg ctg 1173
Tyr Arg Asp Leu Leu Leu Val His Arg Phe Leu Pro Tyr Glu Met Leu
340 345 350

ctc atg tgg gat gcg ctg aac cag ccc aac ctc acc tgc ggc aat cag 1221
Leu Met Trp Asp Ala Leu Asn Gln Pro Asn Leu Thr Cys Gly Asn Gln
355 360 365

aca cag atc tac tgagtcagca tcaggggtccc cagcctctgg gctcctgttt 1273
Thr Gln Ile Tyr
370

ccataggaag gggcgacacc ttctctccag gaagctgaga cctttgtggt ctgagcataa 1333
gggagtgccca gggaagggtt gaggtttgat gagtgaatat tctggctggc gaactcctac 1393
acatccttca aaaccacct ggtactgttc cagcatcttc cctggatggc tggaggaact 1453
ccagaaaata tccatcttct ttttgtggct gctaattggca gaagtgcctg tgctagagtt 1513
ccaactgtgg atgcatccgt cccgtttgag tcaaagtctt acttccctgc tctcacctac 1573
tcacagacgg gatgctaagc agtgcacctg cagtgggtta atggcagata agctccgtct 1633
gcagttccag gccagccaga aactcctgtg tccacataga gctgacgtga gaaatatctt 1693
tcagcccagg agagaggggt cctgatctta accctttcct gggctctcaga caactcagaa 1753
ggttgggggg ataccagaga ggtggtggaa taggaccgcc cctccttac ttgtgggac 1813
aaatgctgta atggtggagg tgtgggcaga ggaggaggc aagtgtcctt tgaaagtgt 1873
gagagctcag agtttctggg gtctcatta ggagccccc tccctgtgtt cccaagaat 1933
tcagagaaca gactggggc tggaatgatc tttaatgggc ccaaggccaa caggcatatg 1993
cctcactact gcctggagaa gggagagatt caggtcctcc agcagcctcc ctcacccagt 2053
atgttttaca gattacgggg ggaccgggtg agccagtgc cccctgcagc cccagcttc 2113
aggcctcagt gtctgccagt caagcttcac aggcattgtg atggggcagc cttggggaat 2173
ataaaatttt gtg 2186

<210> 76
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: restriction
enzyme cleavage sequence

<400> 76
gaattccaca gatcccggt cacgtgggat atccctctc tcct

44

<210> 77
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: fusion protein
start site

<400> 77
Pro Ser Ser Pro
1

<210> 78
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligo DNA
linker

<400> 78
gatcccgggt cacgtgggat

20

<210> 79
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligo DNA
linker

<400> 79
atcccacgtg acccgg

16

<210> 80
<211> 213
<212> PRT
<213> Saccharomyces cerevisiae

<400> 80
Met Asn Lys Glu Ser Lys Asp Asp Asp Met Ser Leu Gly Lys Phe Ser
1 5 10 15

Phe Ser His Phe Leu Tyr Tyr Leu Val Leu Ile Val Val Ile Val Tyr
20 25 30

Gly Leu Tyr Lys Leu Phe Thr Gly His Gly Ser Asp Ile Asn Phe Gly
35 40 45

Lys Phe Leu Leu Arg Thr Ser Pro Tyr Met Trp Ala Asn Leu Gly Ile

50 55 60
Ala Leu Cys Val Gly Leu Ser Val Val Gly Ala Ala Trp Gly Ile Phe
65 70 75 80
Ile Thr Gly Ser Ser Met Ile Gly Ala Gly Val Arg Ala Pro Arg Ile
85 90 95
Thr Thr Lys Asn Leu Ile Ser Ile Ile Phe Cys Glu Val Val Ala Ile
100 105 110
Tyr Gly Leu Ile Ile Ala Ile Val Phe Ser Ser Lys Leu Thr Val Ala
115 120 125
Thr Ala Glu Asn Met Tyr Ser Lys Ser Asn Leu Tyr Thr Gly Tyr Ser
130 135 140
Leu Phe Trp Ala Gly Ile Thr Val Gly Ala Ser Asn Leu Ile Cys Gly
145 150 155 160
Ile Ala Val Gly Ile Thr Gly Ala Thr Ala Ala Ile Ser Asp Ala Ala
165 170 175
Asp Ser Ala Leu Phe Val Lys Ile Leu Val Ile Glu Ile Phe Gly Ser
180 185 190
Ile Leu Gly Leu Leu Gly Leu Ile Val Gly Leu Leu Met Ala Gly Lys
195 200 205
Ala Ser Glu Phe Gln
210

<210> 81
<211> 394
<212> PRT
<213> Rattus sp.

<400> 81
Met Lys Arg Val Ser Trp Ser Leu Gly Thr Ala Ile Leu Pro Gln Thr
1 5 10 15
Leu Ala Ile Leu Trp Gly His Lys Pro Leu Cys Leu Pro Met Phe Ser
20 25 30
Leu Pro Thr Leu Gly Pro His Thr His Arg Pro Leu Ser Ser Pro Leu
35 40 45
Pro Met Val Asn Gln Gly Ile Pro Met Val Pro Val Pro Ile Thr Arg
50 55 60
Trp Leu Pro Leu Lys Asp Leu Leu Lys Glu Ala Thr His Gln Gly His
65 70 75 80
Tyr Pro Gln Ser Pro Phe Pro Pro Asn Pro Tyr Gly Gln Pro Pro Pro
85 90 95

Phe Gln Asp Pro Gly Ser Pro Gln His Gly Asn Tyr Gln Glu Glu Gly
100 105 110

Pro Pro Ser Tyr Tyr Asp Asn Gln Asp Phe Pro Ser Val Asn Trp Asp
115 120 125

Lys Ser Ile Arg Gln Ala Phe Ile Arg Lys Val Phe Leu Val Leu Thr
130 135 140

Leu Gln Leu Ser Val Thr Leu Ser Thr Val Ala Ile Phe Thr Phe Val
145 150 155 160

Gly Glu Val Lys Gly Phe Val Arg Ala Asn Val Trp Thr Tyr Tyr Val
165 170 175

Ser Tyr Ala Ile Phe Phe Ile Ser Leu Ile Val Leu Ser Cys Cys Gly
180 185 190

Asp Phe Arg Lys Lys His Pro Trp Asn Leu Val Ala Leu Ser Ile Leu
195 200 205

Thr Ile Ser Leu Ser Tyr Met Val Gly Met Ile Ala Ser Phe Tyr Asn
210 215 220

Thr Glu Ala Val Ile Met Ala Val Gly Ile Thr Thr Ala Val Cys Phe
225 230 235 240

Thr Val Val Ile Phe Ser Met Gln Thr Arg Tyr Asp Phe Thr Ser Cys
245 250 255

Met Gly Val Leu Leu Val Ser Val Val Val Leu Phe Ile Phe Ala Ile
260 265 270

Leu Cys Ile Phe Ile Arg Asn Arg Ile Leu Glu Ile Val Tyr Ala Ser
275 280 285

Leu Gly Ala Leu Leu Phe Thr Cys Phe Leu Ala Val Asp Thr Gln Leu
290 295 300

Leu Leu Gly Asn Lys Gln Leu Ser Leu Ser Pro Glu Glu Tyr Val Phe
305 310 315 320

Ala Ala Leu Asn Leu Tyr Thr Asp Ile Ile Asn Ile Phe Leu Tyr Ile
325 330 335

Leu Thr Ile Ile Gly Arg Ser Gln Gly Ile Gly Gln Ala Pro Ala Gln
340 345 350

Val Ala Trp Trp Ala Gln Thr His Ala Pro Ala Met Thr Leu Pro Ser
355 360 365

Val Leu Pro Pro Leu Trp Phe Pro Ala Met Ala Trp Ser Arg Gly Ser
370 375 380

Pro Ser Arg Pro Arg Val Cys Thr Leu Gln
385 390

<210> 82
<211> 406
<212> PRT
<213> Bovine Sp.

<400> 82
Val Leu Pro Gln Cys Asn Asp Phe Leu Ser Gln Pro Ala Gly Ser Ala
1 5 10 15
Ala Ser Glu Glu Ser Ser Pro Tyr Cys Ser Asp Ser Arg Gln Leu Arg
20 25 30
Leu Val Asp Gly Gly Gly Pro Cys Gly Gly Arg Val Glu Ile Leu Asp
35 40 45
Gln Gly Ser Trp Gly Thr Ile Cys Asp Asp Asp Trp Asp Leu Asp Asp
50 55 60
Ala Arg Val Val Cys Arg Gln Leu Gly Cys Gly Glu Ala Leu Asn Ala
65 70 75 80
Thr Gly Ser Ala His Phe Gly Ala Gly Ser Gly Pro Ile Trp Leu Asp
85 90 95
Asp Leu Asn Cys Thr Gly Lys Glu Ser His Val Trp Arg Cys Pro Ser
100 105 110
Arg Gly Trp Gly Arg His Asp Cys Arg His Lys Glu Asp Ala Gly Val
115 120 125
Ile Cys Ser Glu Phe Leu Ala Leu Arg Met Val Ser Glu Asp Gln Gln
130 135 140
Cys Ala Gly Trp Leu Glu Val Phe Tyr Asn Gly Thr Trp Gly Ser Val
145 150 155 160
Cys Arg Ser Pro Met Glu Asp Ile Thr Val Ser Val Ile Cys Arg Gln
165 170 175
Leu Gly Cys Gly Asp Ser Gly Ser Leu Asn Thr Ser Val Gly Leu Arg
180 185 190
Glu Gly Ser Arg Pro Arg Trp Val Asp Leu Ile Gln Cys Arg Lys Met
195 200 205
Asp Thr Ser Leu Trp Gln Cys Pro Ser Gly Pro Trp Lys Tyr Ser Ser
210 215 220
Cys Ser Pro Lys Glu Glu Ala Tyr Ile Ser Cys Glu Gly Arg Arg Pro
225 230 235 240
Lys Ser Cys Pro Thr Ala Ala Ala Cys Thr Asp Arg Glu Lys Leu Arg
245 250 255
Leu Arg Gly Gly Asp Ser Glu Cys Ser Gly Arg Val Glu Val Trp His
260 265 270

Asn Gly Ser Trp Gly Thr Val Cys Asp Asp Ser Trp Ser Leu Ala Glu
275 280 285

Ala Glu Val Val Cys Gln Gln Leu Gly Cys Gly Gln Ala Leu Glu Ala
290 295 300

Val Arg Ser Ala Ala Phe Gly Pro Gly Asn Gly Ser Ile Trp Leu Asp
305 310 315 320

Glu Val Gln Cys Gly Gly Arg Glu Ser Ser Leu Trp Asp Cys Val Ala
325 330 335

Glu Pro Trp Gly Gln Ser Asp Cys Lys His Glu Glu Asp Ala Gly Val
340 345 350

Arg Cys Ser Gly Val Arg Thr Thr Leu Pro Thr Thr Thr Ala Gly Thr
355 360 365

Arg Thr Thr Ser Asn Ser Leu Pro Gly Ile Phe Ser Leu Pro Gly Val
370 375 380

Leu Cys Leu Ile Leu Gly Ser Leu Leu Phe Leu Val Leu Val Ile Leu
385 390 395 400

Val Thr Gln Leu Leu Arg
405

<210> 83
<211> 556
<212> PRT
<213> Mus sp.

<400> 83
Met Pro Thr Val Asp Asp Val Leu Glu Gln Val Gly Glu Phe Gly Trp
1 5 10 15

Phe Gln Lys Gln Ala Phe Leu Leu Leu Cys Leu Ile Ser Ala Ser Leu
20 25 30

Ala Pro Ile Tyr Val Gly Ile Val Phe Leu Gly Phe Thr Pro Gly His
35 40 45

Tyr Cys Gln Asn Pro Gly Val Ala Glu Leu Ser Gln Arg Cys Gly Trp
50 55 60

Ser Gln Ala Glu Glu Leu Asn Tyr Thr Val Pro Gly Leu Gly Pro Ser
65 70 75 80

Asp Glu Ala Ser Phe Leu Ser Gln Cys Met Arg Tyr Glu Val Asp Trp
85 90 95

Asn Gln Ser Thr Leu Asp Cys Val Asp Pro Leu Ser Ser Leu Val Ala
100 105 110

Asn Arg Ser Gln Leu Pro Leu Gln Pro Cys Glu His Gly Trp Val Tyr

115 120 125
Asp Thr Pro Gly Ser Ser Ile Val Thr Glu Phe Asn Leu Val Cys Gly
130 135 140
Asp Ala Trp Lys Val Asp Leu Phe Gln Ser Cys Val Asn Leu Gly Phe
145 150 155 160
Phe Leu Gly Ser Leu Val Val Gly Tyr Ile Ala Asp Arg Phe Gly Arg
165 170 175
Lys Leu Cys Leu Leu Val Thr Thr Leu Val Thr Ser Val Ser Gly Val
180 185 190
Leu Thr Ala Val Ala Pro Asp Tyr Thr Ser Met Leu Leu Phe Arg Leu
195 200 205
Leu Gln Gly Met Val Ser Lys Gly Ser Trp Val Ser Gly Tyr Thr Leu
210 215 220
Ile Thr Glu Phe Val Gly Ser Gly Tyr Arg Arg Thr Thr Ala Ile Leu
225 230 235 240
Tyr Gln Met Ala Phe Thr Val Gly Leu Val Gly Leu Ala Gly Val Ala
245 250 255
Tyr Ala Ile Pro Asp Trp Arg Trp Leu Gln Leu Ala Val Ser Leu Pro
260 265 270
Thr Phe Leu Phe Leu Leu Tyr Tyr Trp Phe Val Pro Glu Ser Pro Arg
275 280 285
Trp Leu Leu Ser Gln Lys Arg Thr Thr Arg Ala Val Arg Ile Met Glu
290 295 300
Gln Ile Ala Gln Lys Asn Gly Lys Val Pro Pro Ala Asp Leu Lys Met
305 310 315 320
Leu Cys Leu Glu Glu Asp Ala Ser Glu Lys Arg Ser Pro Ser Phe Ala
325 330 335
Asp Leu Phe Arg Thr Pro Asn Leu Arg Lys His Thr Val Ile Leu Met
340 345 350
Tyr Leu Trp Phe Ser Cys Ala Val Leu Tyr Gln Gly Leu Ile Met His
355 360 365
Val Gly Ala Thr Gly Ala Asn Leu Tyr Leu Asp Phe Phe Tyr Ser Ser
370 375 380
Leu Val Glu Phe Pro Ala Ala Phe Ile Ile Leu Val Thr Ile Asp Arg
385 390 395 400
Ile Gly Arg Ile Tyr Pro Ile Ala Ala Ser Asn Leu Val Thr Gly Ala
405 410 415
Ala Cys Leu Leu Met Ile Phe Ile Pro His Glu Leu His Trp Leu Asn

420 425 430
Val Thr Leu Ala Cys Leu Gly Arg Met Gly Ala Thr Ile Val Leu Gln
435 440 445
Met Val Cys Leu Val Asn Ala Glu Leu Tyr Pro Thr Phe Ile Arg Asn
450 455 460
Leu Gly Met Met Val Cys Ser Ala Leu Cys Asp Leu Gly Gly Ile Phe
465 470 475 480
Thr Pro Phe Met Val Phe Arg Leu Met Glu Val Trp Gln Ala Leu Pro
485 490 495
Leu Ile Leu Phe Gly Val Leu Gly Leu Thr Ala Gly Ala Met Thr Leu
500 505 510
Leu Leu Pro Glu Thr Lys Gly Val Ala Leu Pro Glu Thr Ile Glu Glu
515 520 525
Ala Glu Asn Leu Gly Arg Arg Lys Ser Lys Ala Lys Glu Asn Thr Ile
530 535 540
Tyr Leu Gln Val Gln Thr Gly Lys Ser Ser Ser Thr
545 550 555

<210> 84
<211> 202
<212> PRT
<213> Homo sapiens

<400> 84
Met Cys Tyr Gly Lys Cys Ala Arg Cys Ile Gly His Ser Leu Val Gly
1 5 10 15
Leu Ala Leu Leu Cys Ile Ala Ala Asn Ile Leu Leu Tyr Phe Pro Asn
20 25 30
Gly Glu Thr Lys Tyr Ala Ser Glu Asn His Leu Ser Arg Phe Val Trp
35 40 45
Phe Phe Ser Gly Ile Val Gly Gly Gly Leu Leu Met Leu Leu Pro Ala
50 55 60
Phe Val Phe Ile Gly Leu Glu Gln Asp Asp Cys Cys Gly Cys Cys Gly
65 70 75 80
His Glu Asn Cys Gly Lys Arg Cys Ala Met Leu Ser Ser Val Leu Ala
85 90 95
Ala Leu Ile Gly Ile Ala Gly Ser Gly Tyr Cys Val Ile Val Ala Ala
100 105 110
Leu Gly Leu Ala Glu Gly Pro Leu Cys Leu Asp Ser Leu Gly Gln Trp
115 120 125

Asn Tyr Thr Phe Ala Ser Thr Glu Gly Gln Tyr Leu Leu Asp Thr Ser
130 135 140

Thr Trp Ser Glu Cys Thr Glu Pro Lys His Ile Val Glu Trp Asn Val
145 150 155 160

Ser Leu Phe Ser Ile Leu Leu Ala Leu Gly Gly Ile Glu Phe Ile Leu
165 170 175

Cys Leu Ile Gln Val Ile Asn Gly Val Leu Gly Gly Ile Cys Gly Phe
180 185 190

Cys Cys Ser His Gln Gln Gln Tyr Asp Cys
195 200

<210> 85

<211> 214

<212> PRT

<213> Saccharomyces cerevisiae

<400> 85

Met Ile Thr Ser Phe Leu Met Glu Lys Met Thr Val Ser Ser Asn Tyr
1 5 10 15

Thr Ile Ala Leu Trp Ala Thr Phe Thr Ala Ile Ser Phe Ala Val Gly
20 25 30

Tyr Gln Leu Gly Thr Ser Asn Ala Ser Ser Thr Lys Lys Ser Ser Ala
35 40 45

Thr Leu Leu Arg Ser Lys Glu Met Lys Glu Gly Lys Leu His Asn Asp
50 55 60

Thr Asp Glu Glu Glu Ser Glu Ser Glu Asp Glu Ser Asp Glu Asp Glu
65 70 75 80

Asp Ile Glu Ser Thr Ser Leu Asn Asp Ile Pro Gly Glu Val Arg Met
85 90 95

Ala Leu Val Ile Arg Gln Asp Leu Gly Met Thr Lys Gly Lys Ile Ala
100 105 110

Ala Gln Cys Cys His Ala Ala Leu Ser Cys Phe Arg His Ile Ala Thr
115 120 125

Asn Pro Ala Arg Ala Ser Tyr Asn Pro Ile Met Thr Gln Arg Trp Leu
130 135 140

Asn Ala Gly Gln Ala Lys Ile Thr Leu Lys Cys Pro Asp Lys Phe Thr
145 150 155 160

Met Asp Glu Leu Tyr Ala Lys Ala Ile Ser Leu Gly Val Asn Ala Ala
165 170 175

Val Ile His Asp Ala Gly Arg Thr Gln Ile Ala Ala Gly Ser Ala Thr
180 185 190

Val Leu Gly Leu Gly Pro Ala Pro Lys Ala Val Leu Asp Gln Ile Thr
195 200 205

Gly Asp Leu Lys Leu Tyr
210

<210> 86
<211> 199
<212> PRT
<213> Homo sapiens

<400> 86
Met Ser Ser Glu Asn Cys Phe Val Ala Glu Asn Ser Ser Leu His Pro
1 5 10 15

Glu Ser Gly Gln Glu Asn Asp Ala Thr Ser Pro His Phe Ser Thr Arg
20 25 30

His Glu Gly Ser Phe Gln Val Pro Val Leu Cys Ala Val Met Asn Val
35 40 45

Val Phe Ile Thr Ile Leu Ile Ala Leu Ile Ala Leu Ser Val Gly
50 55 60

Gln Tyr Asn Cys Pro Gly Gln Tyr Thr Phe Ser Met Pro Ser Asp Ser
65 70 75 80

His Val Ser Ser Cys Ser Glu Asp Trp Val Gly Tyr Gln Arg Lys Cys
85 90 95

Tyr Phe Ile Ser Thr Val Lys Arg Ser Trp Thr Ser Ala Gln Asn Ala
100 105 110

Cys Ser Glu His Gly Ala Thr Leu Ala Val Ile Asp Ser Glu Lys Asp
115 120 125

Met Asn Phe Leu Lys Arg Tyr Ala Gly Arg Glu Glu His Trp Val Gly
130 135 140

Leu Lys Lys Glu Pro Gly His Pro Trp Lys Trp Ser Asn Gly Lys Glu
145 150 155 160

Phe Asn Asn Trp Phe Asn Val Thr Gly Ser Asp Lys Cys Val Phe Leu
165 170 175

Lys Asn Thr Glu Val Ser Ser Met Glu Cys Glu Lys Asn Leu Tyr Trp
180 185 190

Ile Cys Asn Lys Pro Tyr Lys
195

<210> 87
<211> 214
<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 87

Met Ile Lys Ser Thr Leu Ile Tyr Arg Glu Asp Gly Leu Pro Leu Cys
1 5 10 15
Thr Ser Val Asp Asn Glu Asn Asp Pro Ser Leu Phe Glu Gln Lys Gln
20 25 30
Lys Val Lys Ile Val Val Ser Arg Leu Thr Pro Gln Ser Ala Thr Glu
35 40 45
Ala Thr Leu Glu Ser Gly Ser Phe Glu Ile His Tyr Leu Lys Lys Ser
50 55 60
Met Val Tyr Tyr Phe Val Ile Cys Glu Ser Gly Tyr Pro Arg Asn Leu
65 70 75 80
Ala Phe Ser Tyr Leu Asn Asp Ile Ala Gln Glu Phe Glu His Ser Phe
85 90 95
Ala Asn Glu Tyr Pro Lys Pro Thr Val Arg Pro Tyr Gln Phe Val Asn
100 105 110
Phe Asp Asn Phe Leu Gln Met Thr Lys Lys Ser Tyr Ser Asp Lys Lys
115 120 125
Val Gln Asp Asn Leu Asp Gln Leu Asn Gln Glu Leu Val Gly Val Lys
130 135 140
Gln Ile Met Ser Lys Asn Ile Glu Asp Leu Leu Tyr Arg Gly Asp Ser
145 150 155 160
Leu Asp Lys Met Ser Asp Met Ser Ser Ser Leu Lys Glu Thr Ser Lys
165 170 175
Arg Tyr Arg Lys Ser Ala Gln Lys Ile Asn Phe Asp Leu Leu Ile Ser
180 185 190
Gln Tyr Ala Pro Ile Val Ile Val Ala Phe Phe Phe Val Phe Leu Phe
195 200 205
Trp Trp Ile Phe Leu Lys
210

<210> 88

<211> 326

<212> PRT

<213> *Homo sapiens*

<400> 88

Met Ala Ser Val Cys Phe Ile Asn Ser Phe Ser Ala Val Leu Gln Gly
1 5 10 15
Ser Leu Phe Gly Gln Leu Gly Thr Met Pro Ser Thr Tyr Ser Thr Leu
20 25 30

Phe Leu Ser Gly Gln Gly Leu Ala Gly Ile Phe Ala Ala Leu Ala Met
35 40 45

Leu Leu Ser Met Ala Ser Gly Val Asp Ala Glu Thr Ser Ala Leu Gly
50 55 60

Tyr Phe Ile Thr Pro Tyr Val Gly Ile Leu Met Ser Ile Val Cys Tyr
65 70 75 80

Leu Ser Leu Pro His Leu Lys Phe Ala Arg Tyr Tyr Leu Ala Asn Lys
85 90 95

Ser Ser Gln Ala Gln Ala Gln Glu Leu Glu Thr Lys Ala Glu Leu Leu
100 105 110

Gln Ser Asp Glu Asn Gly Ile Pro Ser Ser Pro Gln Lys Val Ala Leu
115 120 125

Thr Leu Asp Leu Asp Leu Glu Lys Glu Pro Glu Ser Glu Pro Asp Glu
130 135 140

Pro Gln Lys Pro Gly Lys Pro Ser Val Phe Thr Val Phe Gln Lys Ile
145 150 155 160

Trp Leu Thr Ala Leu Cys Leu Val Leu Val Phe Thr Val Thr Leu Ser
165 170 175

Val Phe Pro Ala Ile Thr Ala Met Val Thr Ser Ser Thr Ser Pro Gly
180 185 190

Lys Trp Ser Gln Phe Phe Asn Pro Ile Cys Cys Phe Leu Leu Phe Asn
195 200 205

Ile Met Asp Trp Leu Gly Arg Ser Leu Thr Ser Tyr Phe Leu Trp Pro
210 215 220

Asp Glu Asp Ser Arg Leu Leu Pro Leu Leu Val Cys Leu Arg Phe Leu
225 230 235 240

Phe Val Pro Leu Phe Met Leu Cys His Val Pro Gln Arg Ser Arg Leu
245 250 255

Pro Ile Leu Phe Pro Gln Asp Ala Tyr Phe Ile Thr Phe Met Leu Leu
260 265 270

Phe Ala Val Ser Asn Gly Tyr Leu Val Ser Leu Thr Met Cys Leu Ala
275 280 285

Pro Arg Gln Val Leu Pro His Glu Arg Glu Val Ala Gly Ala Leu Met
290 295 300

Thr Phe Phe Leu Ala Leu Gly Leu Ser Cys Gly Ala Ser Leu Ser Phe
305 310 315 320

Leu Phe Lys Ala Leu Leu
325

<210> 89
<211> 146
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 89
Met Val Leu Pro Ile Ile Ile Gly Leu Gly Val Thr Met Val Ala Leu
1 5 10 15
Ser Val Lys Ser Gly Leu Asn Ala Trp Thr Val Tyr Lys Thr Leu Ser
20 25 30
Pro Leu Thr Ile Ala Lys Leu Asn Asn Ile Arg Ile Glu Asn Pro Thr
35 40 45
Ala Gly Tyr Arg Asp Ala Leu Lys Phe Lys Ser Ser Leu Ile Asp Glu
50 55 60
Glu Leu Lys Asn Arg Leu Asn Gln Tyr Gln Gly Gly Phe Ala Pro Arg
65 70 75 80
Met Thr Glu Pro Glu Ala Leu Leu Ile Leu Asp Ile Ser Ala Arg Glu
85 90 95
Ile Asn His Leu Asp Glu Lys Leu Leu Lys Lys Lys His Arg Lys Ala
100 105 110
Met Val Arg Asn His Pro Asp Arg Gly Gly Ser Pro Tyr Met Ala Ala
115 120 125
Lys Ile Asn Glu Ala Lys Glu Val Leu Glu Arg Ser Val Leu Leu Arg
130 135 140
Lys Arg
145

<210> 90
<211> 325
<212> PRT
<213> *Drosophila* sp.

<400> 90
Met Gln Ser Lys His Arg Lys Leu Leu Leu Arg Cys Leu Leu Val Leu
1 5 10 15
Pro Leu Ile Leu Leu Val Asp Tyr Cys Gly Leu Leu Thr His Leu His
20 25 30
Glu Leu Asn Phe Glu Arg His Phe His Tyr Pro Leu Asn Asp Asp Thr
35 40 45
Gly Ser Gly Ser Ala Ser Ser Gly Leu Asp Lys Phe Ala Tyr Leu Arg
50 55 60

Val Pro Ser Phe Thr Ala Glu Val Pro Val Asp Gln Pro Ala Arg Leu 80
65 70 75
Thr Met Leu Ile Lys Ser Ala Val Gly Asn Ser Arg Arg Arg Glu Ala 95
85 90
Ile Arg Arg Thr Trp Gly Tyr Glu Gly Arg Phe Ser Asp Val His Leu 110
100 105
Arg Arg Val Phe Leu Leu Gly Thr Ala Glu Asp Ser Glu Lys Asp Val 125
115 120
Ala Trp Glu Ser Arg Glu His Gly Asp Ile Leu Gln Ala Asp Phe Thr 140
130 135
Asp Ala Tyr Phe Asn Asn Thr Leu Lys Thr Met Leu Gly Met Arg Trp 160
145 150
Ala Ser Glu Gln Phe Asn Arg Ser Glu Phe Tyr Leu Phe Val Asp Asp 175
165 170
Asp Tyr Tyr Val Ser Ala Lys Asn Val Leu Lys Phe Leu Gly Arg Gly 190
180 185
Arg Gln Ser His Gln Pro Glu Leu Leu Phe Ala Gly His Val Phe Gln 205
195 200
Thr Ser Pro Leu Arg His Lys Phe Ser Lys Trp Tyr Val Ser Leu Glu 220
210 215
Glu Tyr Pro Phe Asp Arg Trp Pro Pro Tyr Val Thr Ala Gly Ala Phe 240
225 230 235
Ile Leu Ser Gln Lys Ala Leu Arg Gln Leu Tyr Ala Ala Ser Val His 255
245 250
Leu Pro Leu Phe Arg Phe Asp Asp Val Tyr Leu Gly Ile Val Ala Leu 270
260 265
Lys Ala Gly Ile Ser Leu Gln His Cys Asp Asp Phe Arg Phe His Arg 285
275 280
Pro Ala Tyr Lys Gly Pro Asp Ser Tyr Ser Ser Val Ile Ala Ser His 300
290 295
Glu Phe Gly Asp Pro Glu Glu Met Thr Arg Val Trp Asn Glu Cys Arg 320
305 310 315
Ser Ala Asn Tyr Ala 325

<210> 91
<211> 14
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Combined DNA/RNA Molecule:
Nucleotides at positions 12-14 are RNA

<220>

<223> Description of Artificial Sequence: DNA/RNA
chimeric oligonucleotide

<400> 91

ggggaattcg agga

14